



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 100793**

**TO: Maury Audet**  
**Location: CM1/11D04/11D13**  
**Art Unit: 1645**  
**Monday, August 18, 2003**  
  
**Case Serial Number: 09/846779**

**From: Mona Smith**  
**Location: Biotech-Chem Library**  
**CM1-6A01**  
**Phone: 308-3278**  
  
**mona.smith@uspto.gov**

### **Search Notes**

Dear Examiner:

Please see attached results.

Feel free to contact me if you have any questions.

Thank you for using STIC services

Mona Smith  
308-3278

STIC-Biotech/ChemLib

100793

**From:** STIC-ILL  
**Sent:** Monday, August 11, 2003 6:45 AM  
**To:** STIC-Biotech/ChemLib  
**Subject:** FW: Search of SEQ ID NO: 1 (09/846,779)

RECEIVED

AUG 11 2003

(STIC)

-----Original Message-----

**From:** Audet, Maury  
**Sent:** Sunday, August 10, 2003 3:06 PM  
**To:** STIC-ILL  
**Subject:** Search of SEQ ID NO: 1 (09/846,779)

Please search SEQ ID NO: 1 for Ser. No. 09/846,779 (including interfer. files RAPM, RAPN).  
Thanks, Maury

Maury Audet  
Patent Examiner  
Art Unit 1654  
703-305-5039  
11D04

Searcher: M. SMITH  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 8/11/03  
Date Completed: 8/18/03  
Searcher Prep/Review: 3  
Clerical: 2  
Online time: 5

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: 1  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 17, 2003, 23:53:08 ; Search time 69 Seconds  
(without alignments)  
29.905 Million cell updates/sec

Title: US-09-846-779-1  
Perfect score: 77  
Sequence: 1 PNHFRPAGLPEKY 13

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues  
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :			
A_Geneseq_19Jun03.*			
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2:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.*		
3:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.*		
4:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.*		
5:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT.*		
6:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT.*		
7:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT.*		
8:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT.*		
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14:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT.*		
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17:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT.*		
18:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT.*		
19:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT.*		
20:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.*		
21:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.*		
22:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*		
23:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*		
24:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	100.0	13	18 AAW22856	Human serum amyloid
2	77	100.0	13	22 AAB90433	Human SAA amino tr
3	77	100.0	13	22 AAB90534	Human SAA internal
4	77	100.0	14	22 AAB90432	Human SAA amino tr
5	77	100.0	14	22 AAB90533	Human SAA internal
6	77	100.0	15	22 AAB90431	Human SAA amino tr
7	77	100.0	15	22 AAB90532	Human SAA internal
8	77	100.0	16	22 AAB90430	Human SAA amino tr
9	77	100.0	16	22 AAB90531	Human SAA internal

10	77	100.0	17	22 AAB90429	Human SAA amino tr
11	77	100.0	17	22 AAB90530	Human SAA internal
12	77	100.0	18	22 AAB90428	Human SAA amino tr
13	77	100.0	18	22 AAB90529	Human SAA internal
14	77	100.0	19	22 AAB90427	Human SAA amino tr
15	77	100.0	19	22 AAB90528	Human SAA internal
16	77	100.0	20	22 AAB90426	Human SAA amino tr
17	77	100.0	20	22 AAB90527	Human SAA internal
18	77	100.0	21	22 AAB90425	Human SAA amino tr
19	77	100.0	21	22 AAB90526	Human SAA internal
20	77	100.0	22	22 AAB90424	Human SAA amino tr
21	77	100.0	22	22 AAB90525	Human SAA internal
22	77	100.0	23	22 AAB90423	Human SAA amino tr
23	77	100.0	23	22 AAB90524	Human SAA internal
24	77	100.0	24	22 AAB90422	Human SAA amino tr
25	77	100.0	24	22 AAB90523	Human SAA internal
26	77	100.0	25	22 AAB90421	Human SAA amino tr
27	77	100.0	25	22 AAB90522	Human SAA internal
28	77	100.0	26	22 AAB90420	Human SAA amino tr
29	77	100.0	26	22 AAB90521	Human SAA internal
30	77	100.0	27	22 AAB90419	Human SAA amino tr
31	77	100.0	27	22 AAB90520	Human SAA internal
32	77	100.0	28	22 AAB90418	Human SAA amino tr
33	77	100.0	28	22 AAB90519	Human SAA internal
34	77	100.0	29	22 AAB90417	Human SAA amino tr
35	77	100.0	29	22 AAB90518	Human SAA internal
36	77	100.0	30	22 AAB90416	Human SAA amino tr
37	77	100.0	30	22 AAB90517	Human SAA internal
38	77	100.0	31	22 AAB90415	Human SAA amino tr
39	77	100.0	31	22 AAB90516	Human SAA internal
40	77	100.0	32	22 AAB90414	Human SAA amino tr
41	77	100.0	32	22 AAB90515	Human SAA internal
42	77	100.0	33	22 AAB90413	Human SAA amino tr
43	77	100.0	33	22 AAB90514	Human SAA internal
44	77	100.0	34	22 AAB90412	Human SAA amino tr
45	77	100.0	34	22 AAB90513	Human SAA internal

ALIGNMENTS

RESULT 1  
AAW22856  
ID AAW22856 standard; peptide; 13 AA.  
AC AAW22856;  
XX  
DT 18-SEP-1997 (first entry)  
XX  
DE Human serum amyloid A antigen peptide fragment.  
XX  
KW Serum amyloid A; SAA; antigen; antibody; monoclonal; hybridoma;  
KW blood.  
XX  
OS Homo sapiens.  
XX  
RN JP09121888-A.  
XX  
PD 13-MAY-1997.  
XX  
PF 06-NOV-1995; 95JJP-0311531-  
XX  
PR 06-NOV-1995; 95JJP-0311531.  
XX  
PA (MAZN ) COSMO OIL CO-LTD.  
PA (COSM-) COSMO SOGO KENYUSHO KK.  
XX  
WPI; 1997-314238/29.  
XX  
PT Monoclonal antibody specific for human serum amyloid A (SAA) antigen  
PT - used for selective determination of SAA1 and SAA1 des-Arginine in  
PT human blood

PS Example 3; Page 10; 12pp; Japanese.

CC AAW2854-58 are peptide fragments of human serum amyloid A (SAA)  
 CC antigen. The peptides were used to test the selectivity of a new  
 CC monoclonal antibody (SAA03-6) which specifically binds to human serum  
 CC amyloid A antigens SAA1 and SAA1 desArg but does not bind to SAA2 alpha,  
 CC SAA2 alpha-desArg, SAA2 beta and SAA2 beta-desArg. The antibody is used  
 CC for selectively determining the total amount of SAA1 and SAA1 desArg in  
 CC human blood.

XX Sequence 13 AA:

Query Match 100.0%; Score 77; DB 18; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-06;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNHRFPAGLPEKY 13

DB 1 PNHRFPAGLPEKY 13

RESULT 2

AAB90433  
 ID AAB90433 standard; Peptide: 13 AA.

AC AAB90433;

DT 01-JUN-2001 (first entry)

DE Human SAA amino truncation, SEQ ID NO: 191.

KW Human; serum amyloid A; SAA; human formyl peptide receptor variant;  
 KW FPRL1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;  
 KW antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer;  
 KW immune system disorder; amyloidosis; inflammation; infection;  
 KW organ rejection; arthritis; atherosclerosis.

XX Homo sapiens.

OS WO200121188-A1.

PN 29-MAR-2001.

XX 22-SEP-1999; 99WO-US21770.

XX 22-SEP-1999; 99WO-US21770.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;

XX WPI; 2001-211457/21.

XX New serum amyloid A and formyl peptide receptor variant complex and its  
 PT modulators, useful for treating immune system disorders, amyloidosis,  
 PT inflammation, infection, organ rejection, arthritis, atherosclerosis  
 PT and neoplasia.

XX Disclosure; Page 22; 141pp; English.

XX The present sequence is a fragment of human serum amyloid A (SAA). The  
 CC invention relates to the discovery that SAA is a ligand for FPRL1 (human  
 CC formyl peptide receptor variant). A complex has been isolated that  
 CC comprises a peptide agent with a sequence corresponding to SAA, or its  
 CC conservative variant or functional fragment, bound to FPRL1. Modulators  
 CC of the SAA/FPRL1 complex are useful for treating immune system  
 CC disorders, amyloidosis, inflammation, infection, organ rejection,  
 CC arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested  
 CC for their ability to modulate assembly of the SAA/FPRL1 complex.

XX Sequence 13 AA:

Query Match 100.0%; Score 77; DB 22; Length 13;

Best Local Similarity 100.0%; Pred. No. 5.8e-06;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNHRFPAGLPEKY 13

DB 1 PNHRFPAGLPEKY 13

RESULT 3 SAAFAAS 2

AAB90534  
 ID AAB90534 standard; Peptide: 13 AA.

XX AAB90534;

DT 01-JUN-2001 (first entry)

DE Human SAA internal truncation, SEQ ID NO: 292.

KW Human; serum amyloid A; SAA; human formyl peptide receptor variant;  
 KW FPRL1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;  
 KW antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer;  
 KW immune system disorder; amyloidosis; inflammation; infection;  
 KW organ rejection; arthritis; atherosclerosis.

XX Homo sapiens.

OS WO200121188-A1.

PN 29-MAR-2001.

XX 22-SEP-1999; 99WO-US21770.

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 PT inflammation, infection, organ rejection, arthritis, atherosclerosis  
 PT and neoplasia.

XX Disclosure; Page 34; 141pp; English.

XX The present sequence is a fragment of human serum amyloid A (SAA). The  
 CC invention relates to the discovery that SAA is a ligand for FPRL1 (human  
 CC formyl peptide receptor variant). A complex has been isolated that  
 CC comprises a peptide agent with a sequence corresponding to SAA, or its  
 CC conservative variant or functional fragment, bound to FPRL1. Modulators  
 CC of the SAA/FPRL1 complex are useful for treating immune system  
 CC disorders, amyloidosis, inflammation, infection, organ rejection,  
 CC arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested  
 CC for their ability to modulate assembly of the SAA/FPRL1 complex.

XX Sequence 13 AA;

Query Match 100.0%; Score 77; DB 22; Length 13;

Best Local Similarity 100.0%; Pred. No. 5.8e-06;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNHRFPAGLPEKY 13

DB 1 PNHRFPAGLPEKY 13

RESULT 4

AAB90432  
 ID AAB90432 standard; Peptide: 14 AA.

XX AAB90432;

XX 01-JUN-2001 (first entry)  
 XX Human SAA amino truncation, SEQ ID NO: 190.  
 XX  
 XX Human; serum amyloid A; SAA; human formyl peptide receptor variant;  
 KW FPR1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;  
 KW antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer;  
 KW immune system disorder; amyloidosis; inflammation; infection;  
 KW organ rejection; arthritis; atherosclerosis.  
 XX Homo sapiens.  
 OS  
 XX WO200121188-A1.  
 XX  
 XX 29-MAR-2001.  
 XX  
 XX 22-SEP-1999; 99WO-US21770.  
 XX  
 XX 22-SEP-1999; 99WO-US21770.  
 XX  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
 XX WPI; 2001-211457/21.  
 XX  
 XX New serum amyloid A and formyl peptide receptor variant complex and its  
 PT modulators, useful for treating immune system disorders, amyloidosis,  
 PT inflammation, infection, organ rejection, arthritis, atherosclerosis  
 PT and neoplasia -  
 XX  
 XX Disclosure; Page 22; 141pp; English.  
 XX  
 XX The present sequence is a fragment of human serum amyloid A (SAA). The  
 CC invention relates to the discovery that SAA is a ligand for FPRL1 (human  
 CC formyl peptide receptor variant). A complex has been isolated that  
 CC comprises a peptide agent with a sequence corresponding to SAA, or its  
 CC conservative variant or functional fragment, bound to FPRL1. Modulators  
 CC of the SAA/FPRL1 complex are useful for treating immune system  
 CC disorders, amyloidosis, inflammation, infection, organ rejection,  
 CC arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested  
 CC for their ability to modulate assembly of the SAA/FPRL1 complex.  
 XX  
 XX Sequence 14 AA;  
 PS  
 XX Query Match 100.0%; Score 77; DB 22; Length 14;  
 XX Best Local Similarity 100.0%; Pred. No. 6.3e-06;  
 XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PNHFRPAGLPEKY 13  
 DB 2 PNHFRPAGLPEKY 14  
 RESULT 5  
 AAB90533  
 ID AAB90533 standard; Peptide; 14 AA.  
 XX AAB90533;  
 XX  
 XX 01-JUN-2001 (first entry)  
 XX  
 XX Human SAA internal truncation, SEQ ID NO: 291.  
 XX  
 XX Human; serum amyloid A; SAA; human formyl peptide receptor variant;  
 KW FPR1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;  
 KW antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer;  
 KW immune system disorder; amyloidosis; inflammation; infection;  
 KW organ rejection; arthritis; atherosclerosis.  
 XX Homo sapiens.  
 OS  
 XX

PN WO200121188-A1.  
 XX  
 XX 29-MAR-2001.  
 XX  
 XX 22-SEP-1999; 99WO-US21770.  
 XX  
 XX 22-SEP-1999; 99WO-US21770.  
 XX  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
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 XX The present sequence is a fragment of human serum amyloid A (SAA). The  
 CC invention relates to the discovery that SAA is a ligand for FPRL1 (human  
 CC formyl peptide receptor variant). A complex has been isolated that  
 CC comprises a peptide agent with a sequence corresponding to SAA, or its  
 CC conservative variant or functional fragment, bound to FPRL1. Modulators  
 CC of the SAA/FPRL1 complex are useful for treating immune system  
 CC disorders, amyloidosis, inflammation, infection, organ rejection,  
 CC arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested  
 CC for their ability to modulate assembly of the SAA/FPRL1 complex.  
 XX  
 XX Sequence 14 AA;  
 PS  
 XX Query Match 100.0%; Score 77; DB 22; Length 14;  
 XX Best Local Similarity 100.0%; Pred. No. 6.3e-06;  
 XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PNHFRPAGLPEKY 13  
 DB 2 PNHFRPAGLPEKY 14  
 RESULT 6  
 AAB90431  
 ID AAB90431 standard; Peptide; 15 AA.  
 XX AAB90431;  
 XX  
 XX 01-JUN-2001 (first entry)  
 XX  
 XX Human SAA amino truncation, SEQ ID NO: 189.  
 XX  
 XX Human; serum amyloid A; SAA; human formyl peptide receptor variant;  
 KW FPR1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;  
 KW antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer;  
 KW immune system disorder; amyloidosis; inflammation; infection;  
 KW organ rejection; arthritis; atherosclerosis.  
 XX Homo sapiens.  
 OS  
 XX WO200121188-A1.  
 XX  
 XX 29-MAR-2001.  
 XX  
 XX 22-SEP-1999; 99WO-US21770.  
 XX  
 XX 22-SEP-1999; 99WO-US21770.  
 XX  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
 XX WPI; 2001-211457/21.  
 XX  
 XX

xx New serum amyloid A and formyl peptide receptor variant complex and its  
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CC formyl peptide receptor variant). A complex has been isolated that  
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CC conservative variant or functional fragment, bound to FPRL1. Modulators  
CC of the SAA/FPRL1 complex are useful for treating immune system  
CC disorders, amyloidosis, inflammation, infection, organ rejection,  
CC arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested  
CC for their ability to modulate assembly of the SAA/FPRL1 complex.  
xx  
xx Sequence 15 AA;  
xx  
xx Query Match 100.0%; Score 77; DB 22; Length 15;  
xx Best Local Similarity 100.0%; Pred. No. 6.7e-06;  
xx Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
xx  
xx Qy 1 PNHRPAGLPEKY 13  
xx Db 3 PNHRPAGLPEKY 15  
xx  
xx RESULT 7  
xx AAB90532  
xx ID AAB90532 standard; Peptide; 15 AA.  
xx AC AAB90532;  
xx XX  
xx DT 01-JUN-2001 (first entry)  
xx DE Human SAA internal truncation, SEQ ID NO: 290.  
xx  
xx Human; serum amyloid A; SAA; human formyl peptide receptor variant;  
xx FPRL1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;  
xx antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer;  
xx immune system disorder; amyloidosis; inflammation; infection;  
xx organ rejection; arthritis; atherosclerosis.  
xx  
xx OS Homo sapiens.  
xx XX  
xx PN WO200121188-A1.  
xx PD 29-MAR-2001.  
xx PF 22-SEP-1999; 99WO-US21770.  
xx PR 22-SEP-1999; 99WO-US21770.  
xx XX  
xx PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
xx PI Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
xx WPI; 2001-211457/21.  
xx  
xx New serum amyloid A and formyl peptide receptor variant complex and its  
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CC disorders, amyloidosis, inflammation, infection, organ rejection,  
CC arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested  
CC for their ability to modulate assembly of the SAA/FPRL1 complex.  
xx  
xx Sequence 15 AA;  
xx  
xx Query Match 100.0%; Score 77; DB 22; Length 15;  
xx Best Local Similarity 100.0%; Pred. No. 6.7e-06;  
xx Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
xx  
xx Qy 1 PNHRPAGLPEKY 13  
xx Db 3 PNHRPAGLPEKY 15  
xx  
xx RESULT 8  
xx AAB90430  
xx ID AAB90430 standard; Peptide; 16 AA.  
xx AC AAB90430;  
xx XX  
xx DT 01-JUN-2001 (first entry)  
xx DE Human SAA amino truncation, SEQ ID NO: 188.  
xx  
xx Human; serum amyloid A; SAA; human formyl peptide receptor variant;  
xx FPRL1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;  
xx antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer;  
xx immune system disorder; amyloidosis; inflammation; infection;  
xx organ rejection; arthritis; atherosclerosis.  
xx  
xx OS Homo sapiens.  
xx XX  
xx PN WO200121188-A1.  
xx PD 29-MAR-2001.  
xx PF 22-SEP-1999; 99WO-US21770.  
xx PR 22-SEP-1999; 99WO-US21770.  
xx XX  
xx PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
xx PI Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
xx WPI; 2001-211457/21.  
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CC disorders, amyloidosis, inflammation, infection, organ rejection,  
CC arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested  
CC for their ability to modulate assembly of the SAA/FPRL1 complex.  
xx  
xx Sequence 16 AA;  
xx  
xx Query Match 100.0%; Score 77; DB 22; Length 16;  
xx Best Local Similarity 100.0%; Pred. No. 7.2e-06;  
xx Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
xx  
xx Qy 1 PNHRPAGLPEKY 13  
xx Db 3 PNHRPAGLPEKY 15

Db 4 PNHFRPAGLPEKY 16  
 RESULT 9  
 AAB90531  
 ID AAB90531 standard; Peptide: 16 AA.  
 XX  
 XX AAB90531;  
 AC  
 XX 01-JUN-2001 (first entry)  
 DT  
 XX Human SAA internal truncation, SEQ ID NO: 289.  
 DE  
 XX Human; serum amyloid A; SAA; human formyl peptide receptor variant;  
 KW FPR1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;  
 KW antiatherosclerotic; immunosuppressive; SAA/FPR1 complex; cancer;  
 KW immune system disorder; amyloidosis; inflammation; infection;  
 KW organ rejection; arthritis; atherosclerosis.  
 YX  
 XX Homo sapiens.  
 S  
 XX WO200121188-A1.  
 PN  
 XX 29-MAR-2001.  
 PD  
 XX 22-SEP-1999; 99WO-US21770.  
 PF  
 XX 22-SEP-1999; 99WO-US21770.  
 PP  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA  
 XX Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
 PI WPI; 2001-211457/21.  
 XX  
 XX New serum amyloid A and formyl peptide receptor variant complex and its  
 PT modulators, useful for treating immune system disorders, amyloidosis,  
 PT inflammation, infection, organ rejection, arthritis, atherosclerosis  
 PT and neoplasia  
 XX  
 PS Disclosure; Page 22; 141pp; English.  
 XX  
 CC The present sequence is a fragment of human serum amyloid A (SAA). The  
 CC invention relates to the discovery that SAA is a ligand for FPR1 (human  
 CC formyl peptide receptor variant). A complex has been isolated that  
 CC comprises a peptide agent with a sequence corresponding to SAA, or its  
 CC conservative variant or functional fragment, bound to FPR1. Modulators  
 CC of the SAA/FPR1 complex are useful for treating immune system  
 CC disorders, amyloidosis, inflammation, infection, organ rejection,  
 CC arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested  
 CC for their ability to modulate assembly of the SAA/FPR1 complex.  
 XX  
 PS Sequence 16 AA;  
 XX  
 XX Query Match 100.0%; Score 77; DB 22; Length 16;  
 XX Best Local Similarity 100.0%; Pred. No. 7.2e-06;  
 XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PNHFRPAGLPEKY 13  
 DB 4 PNHFRPAGLPEKY 16  
 |||||||||  
 |||||||||  
 RESULT 10  
 AAB90429  
 ID AAB90429 standard; Peptide: 17 AA.  
 XX  
 XX AAB90429;  
 AC  
 XX 01-JUN-2001 (first entry)  
 DT  
 XX Human SAA amino truncation, SEQ ID NO: 187.  
 DE  
 XX Human; serum amyloid A; SAA; human formyl peptide receptor variant;  
 KW FPR1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;  
 KW antiatherosclerotic; immunosuppressive; SAA/FPR1 complex; cancer;  
 KW immune system disorder; amyloidosis; inflammation; infection;  
 KW organ rejection; arthritis; atherosclerosis.  
 YX  
 XX Homo sapiens.  
 S  
 XX WO200121188-A1.  
 PN  
 XX 29-MAR-2001.  
 PD  
 XX 22-SEP-1999; 99WO-US21770.  
 PF  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA  
 XX Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
 PI WPI; 2001-211457/21.  
 XX  
 XX New serum amyloid A and formyl peptide receptor variant complex and its  
 PT modulators, useful for treating immune system disorders, amyloidosis,  
 PT inflammation, infection, organ rejection, arthritis, atherosclerosis  
 PT and neoplasia  
 XX  
 PS Disclosure; Page 34; 141pp; English.  
 XX  
 CC The present sequence is a fragment of human serum amyloid A (SAA). The  
 CC invention relates to the discovery that SAA is a ligand for FPR1 (human  
 CC formyl peptide receptor variant). A complex has been isolated that  
 CC comprises a peptide agent with a sequence corresponding to SAA, or its  
 CC conservative variant or functional fragment, bound to FPR1. Modulators  
 CC of the SAA/FPR1 complex are useful for treating immune system  
 CC disorders, amyloidosis, inflammation, infection, organ rejection,  
 CC arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested  
 CC for their ability to modulate assembly of the SAA/FPR1 complex.  
 XX  
 PS Sequence 17 AA;  
 XX  
 XX Query Match 100.0%; Score 77; DB 22; Length 17;  
 XX Best Local Similarity 100.0%; Pred. No. 7.6e-06;  
 XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PNHFRPAGLPEKY 13  
 DB 5 PNHFRPAGLPEKY 17  
 |||||||||  
 |||||||||  
 RESULT 11  
 AAB90530  
 ID AAB90530 standard; Peptide: 17 AA.  
 XX  
 XX AAB90530;  
 AC  
 XX 01-JUN-2001 (first entry)  
 DT  
 XX Human SAA internal truncation, SEQ ID NO: 289.  
 DE  
 XX Human; serum amyloid A; SAA; human formyl peptide receptor variant;  
 KW FPR1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;  
 KW antiatherosclerotic; immunosuppressive; SAA/FPR1 complex; cancer;  
 KW immune system disorder; amyloidosis; inflammation; infection;  
 KW organ rejection; arthritis; atherosclerosis.  
 YX  
 XX Homo sapiens.  
 S  
 XX WO200121188-A1.  
 PN  
 XX 29-MAR-2001.  
 PD  
 XX 22-SEP-1999; 99WO-US21770.  
 PF

XX 22-SEP-1999; 99WO-US21770.  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
 XX WPI; 2001-211457/21.  
 XX New serum amyloid A and formyl peptide receptor variant complex and its  
 PT modulators, useful for treating immune system disorders, amyloidosis,  
 PT inflammation, infection, organ rejection, arthritis, atherosclerosis  
 PT and neoplasia -  
 XX  
 XX Disclosure; Page 34; 141pp; English.  
 XX The present sequence is a fragment of human serum amyloid A (SAA). The  
 CC invention relates to the discovery that SAA is a ligand for FPRL1 (human  
 CC formyl peptide receptor variant). A complex has been isolated that  
 CC comprises a peptide agent with a sequence corresponding to SAA, or its  
 CC conservative variant or functional fragment, bound to FPRL1. Modulators  
 CC of the SAA/FPRL1 complex are useful for treating immune system  
 CC disorders, amyloidosis, inflammation, infection, organ rejection,  
 CC arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested  
 CC for their ability to modulate assembly of the SAA/FPRL1 complex.  
 XX  
 XX Sequence 17 AA:  
 PS Query Match 100.0%; Score 77; DB 22; Length 17;  
 XX Best Local Similarity 100.0%; Pred. No. 7.6e-06;  
 XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PNHFRPAGLPEKY 13  
 DB 5 PNHFRPAGLPEKY 17  
 RESULT 12  
 AAB90428  
 ID AAB90428 standard; Peptide; 18 AA.  
 XX AAB90428;  
 XX  
 XX 01-JUN-2001 (first entry)  
 XX Human SAA amino truncation, SEQ ID NO: 186.  
 XX Human; serum amyloid A; SAA; human formyl peptide receptor variant;  
 KW FPRL1; immunomodulatory; antinflammatory; antimicrobial; antiarthritic;  
 KW antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer;  
 Y immune system disorder; amyloidosis; inflammation; infection;  
 W organ rejection; arthritis; atherosclerosis.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200121188-A1.  
 PN  
 XX 29-MAR-2001.  
 XX 22-SEP-1999; 99WO-US21770.  
 XX 22-SEP-1999; 99WO-US21770.  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
 XX WPI; 2001-211457/21.  
 XX New serum amyloid A and formyl peptide receptor variant complex and its  
 PT modulators, useful for treating immune system disorders, amyloidosis,  
 PT inflammation, infection, organ rejection, arthritis, atherosclerosis  
 PT and neoplasia -

XX Disclosure; Page 22; 141pp; English.  
 XX The present sequence is a fragment of human serum amyloid A (SAA). The  
 CC invention relates to the discovery that SAA is a ligand for FPRL1 (human  
 CC formyl peptide receptor variant). A complex has been isolated that  
 CC comprises a peptide agent with a sequence corresponding to SAA, or its  
 CC conservative variant or functional fragment, bound to FPRL1. Modulators  
 CC of the SAA/FPRL1 complex are useful for treating immune system  
 CC disorders, amyloidosis, inflammation, infection, organ rejection,  
 CC arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested  
 CC for their ability to modulate assembly of the SAA/FPRL1 complex.  
 XX  
 XX Sequence 18 AA;  
 PS Query Match 100.0%; Score 77; DB 22; Length 18;  
 XX Best Local Similarity 100.0%; Pred. No. 8.1e-06;  
 XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PNHFRPAGLPEKY 13  
 DB 6 PNHFRPAGLPEKY 18  
 RESULT 13  
 AAB90529  
 ID AAB90529 standard; Peptide; 18 AA.  
 XX AAB90529;  
 XX  
 XX 01-JUN-2001 (first entry)  
 XX Human SAA internal truncation, SEQ ID NO: 287.  
 XX Human; serum amyloid A; SAA; human formyl peptide receptor variant;  
 KW FPRL1; immunomodulatory; antinflammatory; antimicrobial; antiarthritic;  
 KW antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer;  
 KW immune system disorder; amyloidosis; inflammation; infection;  
 KW organ rejection; arthritis; atherosclerosis.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200121188-A1.  
 PN  
 XX 29-MAR-2001.  
 XX 22-SEP-1999; 99WO-US21770.  
 XX 22-SEP-1999; 99WO-US21770.  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
 XX WPI; 2001-211457/21.  
 XX New serum amyloid A and formyl peptide receptor variant complex and its  
 PT modulators, useful for treating immune system disorders, amyloidosis,  
 PT inflammation, infection, organ rejection, arthritis, atherosclerosis  
 PT and neoplasia -  
 XX  
 XX Disclosure; Page 34; 141pp; English.  
 XX The present sequence is a fragment of human serum amyloid A (SAA). The  
 CC invention relates to the discovery that SAA is a ligand for FPRL1 (human  
 CC formyl peptide receptor variant). A complex has been isolated that  
 CC comprises a peptide agent with a sequence corresponding to SAA, or its  
 CC conservative variant or functional fragment, bound to FPRL1. Modulators  
 CC of the SAA/FPRL1 complex are useful for treating immune system  
 CC disorders, amyloidosis, inflammation, infection, organ rejection,  
 CC arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested  
 CC for their ability to modulate assembly of the SAA/FPRL1 complex.  
 XX



SQ Sequence 18 AA;

Query Match 100.0%; Score 77; DB 22; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-06;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNHRPAGLPEKY 13  
 I|||||  
 DB 6 PNHRPAGLPEKY 18

RESULT 14

AAB90427

ID AAB90427 standard; Peptide; 19 AA.  
 AC AAB90427;  
 XX  
 XX 01-JUN-2001 (first entry)  
 DT Human SAA amino truncation, SEQ ID NO: 185.  
 DE  
 XX Human; serum amyloid A; SAA; human formyl peptide receptor variant;  
 KW FPR1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;  
 KW antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer;  
 KW immune system disorder; amyloidosis; inflammation; infection;  
 KW organ rejection; arthritis; atherosclerosis.  
 XX Homo sapiens.  
 OS  
 XX WO200121188-A1.  
 PN  
 XX 29-MAR-2001.  
 PD  
 XX 22-SEP-1999; 99WO-US21770.  
 PF  
 XX 22-SEP-1999; 99WO-US21770.  
 PR  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
 PI WPI; 2001-211457/21.  
 DR  
 XX New serum amyloid A and formyl peptide receptor variant complex and its  
 PT modulators, useful for treating immune system disorders, amyloidosis,  
 PT inflammation, infection, organ rejection, arthritis, atherosclerosis  
 PT and neoplasia -  
 XX  
 PS Disclosure; Page 22; 141pp; English.

XX The present sequence is a fragment of human serum amyloid A (SAA). The  
 CC invention relates to the discovery that SAA is a ligand for FPRL1 (human  
 CC formyl peptide receptor variant). A complex has been isolated that  
 CC comprises a peptide agent with a sequence corresponding to SAA, or its  
 CC conservative variant or functional fragment, bound to FPRL1. Modulators  
 CC of the SAA/FPRL1 complex are useful for treating immune system  
 CC disorders, amyloidosis, inflammation, infection, organ rejection,  
 CC arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested  
 CC for their ability to modulate assembly of the SAA/FPRL1 complex.  
 XX  
 SQ Sequence 19 AA;

Query Match 100.0%; Score 77; DB 22; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 8.5e-06;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNHRPAGLPEKY 13  
 I|||||  
 DB 7 PNHRPAGLPEKY 19

RESULT 15

AAB90528

Query Match 100.0%; Score 77; DB 22; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 8.5e-06;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNHRPAGLPEKY 13  
 I|||||  
 DB 7 PNHRPAGLPEKY 19

AAB90528 standard; Peptide; 19 AA.

AAB90528;

01-JUN-2001 (first entry)

Human SAA internal truncation, SEQ ID NO: 286.

Human; serum amyloid A; SAA; human formyl peptide receptor variant;  
 FPRL1; immunomodulatory; antiinflammatory; antimicrobial; antiarthritic;  
 KW antiatherosclerotic; immunosuppressive; SAA/FPRL1 complex; cancer;  
 KW immune system disorder; amyloidosis; inflammation; infection;  
 KW organ rejection; arthritis; atherosclerosis.

Homo sapiens.

WO200121188-A1.

29-MAR-2001.

22-SEP-1999; 99WO-US21770.

22-SEP-1999; 99WO-US21770.

(USSH ) US DEPT HEALTH &amp; HUMAN SERVICES.

Wang J, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;

WPI; 2001-211457/21.

New serum amyloid A and formyl peptide receptor variant complex and its  
 modulators, useful for treating immune system disorders, amyloidosis,  
 inflammation, infection, organ rejection, arthritis, atherosclerosis  
 and neoplasia -

Disclosure; Page 33; 141pp; English.

The present sequence is a fragment of human serum amyloid A (SAA). The  
 invention relates to the discovery that SAA is a ligand for FPRL1 (human  
 formyl peptide receptor variant). A complex has been isolated that  
 comprises a peptide agent with a sequence corresponding to SAA, or its  
 conservative variant or functional fragment, bound to FPRL1. Modulators  
 of the SAA/FPRL1 complex are useful for treating immune system  
 disorders, amyloidosis, inflammation, infection, organ rejection,  
 arthritis, atherosclerosis and neoplasia. Fragments of SAA were tested  
 for their ability to modulate assembly of the SAA/FPRL1 complex.

Sequence 19 AA;

Query Match 100.0%; Score 77; DB 22; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 8.5e-06;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNHRPAGLPEKY 13  
 I|||||  
 DB 7 PNHRPAGLPEKY 19

Search completed: August 18, 2003, 01:24:05  
 Job time : 69 secs

RESULT 2  
US-10-099-782A-292  
; Sequence 292, Application US/10099782A

; CURRENT FILING DATE: 2002-10-25  
; PRIOR APPLICATION NUMBER: PCT/US99/21770  
; PRIOR FILING DATE: 1999-09-22  
; NUMBER OF SEQ ID NOS: 301  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 288  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-099-782A-288

Query Match 100.0%; Score 77; DB 15; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.7e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNHRPAGLPEKY 13  
| | | | | | | | | | | | | | |  
DB 5 PNHRPAGLPEKY 17

RESULT 11  
US-10-099-782A-186  
; Sequence 186, Application US/10099782A  
; Publication No. US20030120037A1  
; GENERAL INFORMATION:  
; APPLICANT: Ji-Ming Wang  
; APPLICANT: Joost J. Oppenheim  
; APPLICANT: Shao-Bo Su  
; APPLICANT: Wang-Hua Gong  
; APPLICANT: Ji-Liang Gao  
; APPLICANT: Philip M. Murphy  
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL  
; TITLE OF INVENTION: RECEPTOR BY SERUM AMYLOID A (SAA)  
; FILE REFERENCE: NIH173.001C1  
; CURRENT APPLICATION NUMBER: US/10/099,782A  
; CURRENT FILING DATE: 2002-10-25  
; PRIOR APPLICATION NUMBER: PCT/US99/21770  
; PRIOR FILING DATE: 1999-09-22  
; NUMBER OF SEQ ID NOS: 301  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 186  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-099-782A-186

Query Match 100.0%; Score 77; DB 15; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNHRPAGLPEKY 13  
| | | | | | | | | | | | | | |  
DB 6 PNHRPAGLPEKY 18

RESULT 12  
US-10-099-782A-287  
; Sequence 287, Application US/10099782A  
; Publication No. US20030120037A1  
; GENERAL INFORMATION:  
; APPLICANT: Ji-Ming Wang  
; APPLICANT: Joost J. Oppenheim  
; APPLICANT: Shao-Bo Su  
; APPLICANT: Wang-Hua Gong  
; APPLICANT: Ji-Liang Gao  
; APPLICANT: Philip M. Murphy  
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL  
; TITLE OF INVENTION: RECEPTOR BY SERUM AMYLOID A (SAA)  
; FILE REFERENCE: NIH173.001C1  
; CURRENT APPLICATION NUMBER: US/10/099,782A  
; CURRENT FILING DATE: 2002-10-25  
; PRIOR APPLICATION NUMBER: PCT/US99/21770  
; PRIOR FILING DATE: 1999-09-22

; NUMBER OF SEQ ID NOS: 301  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 287  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-099-782A-287

Query Match 100.0%; Score 77; DB 15; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNHRPAGLPEKY 13  
| | | | | | | | | | | | | | |  
DB 6 PNHRPAGLPEKY 18

RESULT 13  
US-10-099-782A-185  
; Sequence 185, Application US/10099782A  
; Publication No. US20030120037A1  
; GENERAL INFORMATION:  
; APPLICANT: Ji-Ming Wang  
; APPLICANT: Joost J. Oppenheim  
; APPLICANT: Shao-Bo Su  
; APPLICANT: Wang-Hua Gong  
; APPLICANT: Ji-Liang Gao  
; APPLICANT: Philip M. Murphy  
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL  
; TITLE OF INVENTION: RECEPTOR BY SERUM AMYLOID A (SAA)  
; FILE REFERENCE: NIH173.001C1  
; CURRENT APPLICATION NUMBER: US/10/099,782A  
; CURRENT FILING DATE: 2002-10-25  
; PRIOR APPLICATION NUMBER: PCT/US99/21770  
; PRIOR FILING DATE: 1999-09-22  
; NUMBER OF SEQ ID NOS: 301  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 185  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-099-782A-185

Query Match 100.0%; Score 77; DB 15; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.4e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNHRPAGLPEKY 13  
| | | | | | | | | | | | | | |  
DB 7 PNHRPAGLPEKY 19

RESULT 14  
US-10-099-782A-286  
; Sequence 286, Application US/10099782A  
; Publication No. US20030120037A1  
; GENERAL INFORMATION:  
; APPLICANT: Ji-Ming Wang  
; APPLICANT: Joost J. Oppenheim  
; APPLICANT: Shao-Bo Su  
; APPLICANT: Wang-Hua Gong  
; APPLICANT: Ji-Liang Gao  
; APPLICANT: Philip M. Murphy  
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL  
; TITLE OF INVENTION: RECEPTOR BY SERUM AMYLOID A (SAA)  
; FILE REFERENCE: NIH173.001C1  
; CURRENT APPLICATION NUMBER: US/10/099,782A  
; CURRENT FILING DATE: 2002-10-25  
; PRIOR APPLICATION NUMBER: PCT/US99/21770  
; PRIOR FILING DATE: 1999-09-22  
; NUMBER OF SEQ ID NOS: 301  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 286

; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-099-782A-286

Query Match 100.0%; Score 77; DB 15; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.4e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNHFRPAGLPEKY 13  
Db 7 PNHFRPAGLPEKY 19

RESULT 15

US-10-099-782A-184  
; Sequence 184, Application US/10099782A  
; Publication No. US20030120037A1  
; GENERAL INFORMATION:  
; APPLICANT: Ji-Ming Wang  
; APPLICANT: Joost J. Oppenheim  
; APPLICANT: Shao-Bo Su  
; APPLICANT: Wang-Hua Gong  
; APPLICANT: Ji-Liang Gao  
; APPLICANT: Philip M. Murphy  
; TITLE OF INVENTION: UTILIZATION OF FPR1 AS A FUNCTIONAL  
; FILE REFERENCE: NIH173.001C1  
; CURRENT APPLICATION NUMBER: US/10/099,782A  
; PRIOR FILING DATE: 2002-10-25  
; PRIOR APPLICATION NUMBER: PCT/US99/21770  
; PRIOR FILING DATE: 1999-09-22  
; NUMBER OF SEQ ID NOS: 301  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 184  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-099-782A-184

Query Match 100.0%; Score 77; DB 15; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.7e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNHFRPAGLPEKY 13  
Db 8 PNHFRPAGLPEKY 20

Search completed: August 18, 2003, 01:34:56  
Job time : 52 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 18, 2003, 01:22:53 ; Search time 42 Seconds  
(without alignments)  
13.09% Million cell updates/sec

Title: US-09-846-779-1

Perfect score: 77

Sequence: 1 PNHFRPAGLPEKY 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.AA.\*

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	122	4	US-09-154-750A-82
2	71	92.2	129	4	US-09-425-679E-11
3	68	88.3	117	4	US-09-425-679E-8
4	68	88.3	104	4	US-09-029-345-1
5	68	88.3	110	4	US-09-425-679E-10
6	45	58.4	112	3	US-09-240-274-64
7	42	54.5	845	4	US-09-252-991A-17856
8	40	51.9	109	3	US-09-240-274-61
9	40	51.9	363	4	US-09-252-991A-19920
10	40	51.9	497	4	US-09-252-991A-23620
11	40	51.9	762	4	US-09-252-991A-29423
12	39	50.6	109	2	US-08-672-345C-3
13	39	50.6	109	2	US-08-672-345C-93
14	39	50.6	109	3	US-08-214-095D-3
15	39	50.6	109	3	US-08-214-095D-121
16	39	50.6	111	3	US-08-983-607-35
17	39	50.6	112	3	US-08-983-607-31
18	39	50.6	112	3	US-08-983-607-49
19	39	50.6	114	3	US-09-240-274-62
20	39	50.6	123	4	US-09-996-243-117
21	39	50.6	132	2	US-08-345-321-4
22	39	50.6	181	4	US-09-252-991A-23085
23	39	50.6	234	4	US-09-372-425A-4
24	39	50.6	503	4	US-09-252-991A-32663
25	39	50.6	680	1	US-08-211-430-2
26	39	50.6	680	3	US-08-761-136-1
27	39	50.6	680	4	US-09-576-967-1

Sequence 111, Appl  
Sequence 38, Appl  
Sequence 38, Appl  
Sequence 16, Appl  
Sequence 16, Appl  
Sequence 34, Appl  
Sequence 55, Appl  
Sequence 12, Appl  
Sequence 12, Appl  
Sequence 12, Appl  
Sequence 12, Appl  
Sequence 20, Appl  
Sequence 12, Appl  
Sequence 91, Appl  
Sequence 91, Appl  
Sequence 2, Appl  
Sequence 54, Appl  
Sequence 57, Appl

#### ALIGNMENTS

RESULT 1  
US-09-154-750A-82  
; Sequence 82, Application US/09154750A  
; Patent No. 6432640  
; GENERAL INFORMATION:  
; APPLICANT: Vogelstein, Bert  
; APPLICANT: Kinzler, Kenneth  
; APPLICANT: Polyak, Kornelia  
; TITLE OF INVENTION: p53-Induced Apoptosis  
; FILE REFERENCE: 1107.75357  
; CURRENT APPLICATION NUMBER: US/09/154,750A  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/059,153  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/079817  
; PRIOR FILING DATE: 1998-03-30  
; NUMBER OF SEQ ID NOS: 93  
; SOFTWARE: fastseq for Windows Version 3.0  
; SEQ ID NO 82  
; LENGTH: 122  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-154-750A-82

Query Match Similarity 100.0%; Score 77; DB 4; Length 122;  
Best Local Similarity 100.0%; Pred. No. 1.8e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNHFRPAGLPEKY 13  
DB 110 PNHFRPAGLPEKY 122

RESULT 2  
US-09-425-679E-11  
; Sequence 11, Application US/09425679E  
; Patent No. 6509444  
; GENERAL INFORMATION:  
; APPLICANT: McDonald, Thomas L.  
; APPLICANT: Weber, Annika L.  
; TITLE OF INVENTION: Serum Amyloid A Isoform from Colostrum  
; FILE REFERENCE: UMC 63142  
; CURRENT APPLICATION NUMBER: US/09/425,679E  
; CURRENT FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: US 60/218,482  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/218,611  
; PRIOR FILING DATE: 2000-07-17  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 11
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mustela vison
US-09-425-679E-11

Query Match      92.2%; Score 71; DB 4; Length 129;
Best Local Similarity 84.6%; Pred. No. 0.00018;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNHFRPAGLPKY 13
Db 117 PNHFRPSGLPKY 129

RESULT 3
US-09-425-679E-8
; Sequence 8, Application US/09425679E
; Patent No. 6509444
; GENERAL INFORMATION:
; APPLICANT: McDonald, Thomas L.
; TITLE OF INVENTION: Serum Amyloid A Isoform from Colostrum
; FILE REFERENCE: UNMC 63142
; CURRENT APPLICATION NUMBER: US/09/425,679E
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US 60/218,482
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/218,611
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Equus caballus
US-09-425-679E-8

Query Match      88.3%; Score 68; DB 4; Length 17;
Best Local Similarity 84.6%; Pred. No. 6.6e-05;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PNHFRPAGLPKY 13
Db 5 PNHFRPHGLPKY 17

RESULT 4
US-09-029-345-1
; Sequence 1, Application US/09029345B
; Patent No. 6375949
; GENERAL INFORMATION:
; APPLICANT: Hirano, et al.
; TITLE OF INVENTION: Monoclonal Antibody Recognizing Serum Amyloid A
; FILE REFERENCE: 112842-100
; CURRENT APPLICATION NUMBER: US/09/029,345B
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-029-345-1

Query Match      88.3%; Score 68; DB 4; Length 104;
Best Local Similarity 92.3%; Pred. No. 0.00044;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PNHFRPAGLPKY 13
Db 92 PNHDRPAGLPKY 104

us-09-846-779-1.ra1

RESULT 5
US-09-425-679E-10
; Sequence 10, Application US/09425679E
; Patent No. 6509444
; GENERAL INFORMATION:
; APPLICANT: McDonald, Thomas L.
; APPLICANT: Weber, Annika L.
; TITLE OF INVENTION: Serum Amyloid A Isoform from Colostrum
; FILE REFERENCE: UNMC 63142
; CURRENT APPLICATION NUMBER: US/09/425,679E
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US 60/218,482
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/218,611
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Equus caballus
US-09-425-679E-10

Query Match      88.3%; Score 68; DB 4; Length 110;
Best Local Similarity 84.6%; Pred. No. 0.00047;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PNHFRPAGLPKY 13
Db 98 PNHFRPHGLPKY 110

RESULT 6
US-09-240-274-64
; Sequence 64, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 002
US-09-240-274-64

Query Match      58.4%; Score 45; DB 3; Length 112;
Best Local Similarity 50.0%; Pred. No. 2.6;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 PNHFRPAGLPKY 13
Db 52 PNHFRPSGLPKY 63

RESULT 7
US-09-252-991A-17856
; Sequence 17856, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
```

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252.991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 17856  
; LENGTH: 845  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-17856

Query Match 54.5%; Score 42; DB 4; Length 845;  
Best Local Similarity 80.0%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PNHRPAGLP 10  
| | | | | | | |  
DB 267 PLHRRPAGLP 276

RESULT 8  
US-09-240-274-61  
; Sequence 61, Application US/09240274  
; Patent No. 6255455  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-4202  
; CURRENT APPLICATION NUMBER: US/09/240,274  
; CURRENT FILING DATE: 1999-01-29  
; EARLIER APPLICATION NUMBER: 60/081,380  
; EARLIER FILING DATE: 1998-04-10  
; EARLIER APPLICATION NUMBER: 60/028,550  
; EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 61  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) chain N01  
US-09-240-274-61

Query Match 51.9%; Score 40; DB 3; Length 109;  
Best Local Similarity 41.7%; Pred. No. 16;  
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 NHRFPAGLP 13  
| | | | | | | |  
DB 51 NYRRPSGIPDRF 62

RESULT 9  
US-09-252-991A-19920  
; Sequence 19920, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252.991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 29423  
; LENGTH: 762  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-29423

Query Match 51.9%; Score 40; DB 4; Length 762;  
Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
Matches 8; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 19920  
; LENGTH: 363  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-19920

Query Match 51.9%; Score 40; DB 4; Length 363;  
Best Local Similarity 41.7%; Pred. No. 58;  
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 PNHRPAGLP 12  
| | | | | | | |  
DB 209 PHLQPVGVPRR 220

## RESULT 10

US-09-252-991A-23620  
; Sequence 23620, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252.991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 23620  
; LENGTH: 497  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-23620

Query Match 51.9%; Score 40; DB 4; Length 497;  
Best Local Similarity 53.8%; Pred. No. 80;  
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 PNHRPAGLP 13  
| | | | | | | |  
DB 174 PGRGRPAALPRRY 186

## RESULT 11

US-09-252-991A-29423  
; Sequence 29423, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252.991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 29423  
; LENGTH: 762  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-29423

Query Match 51.9%; Score 40; DB 4; Length 762;  
Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
Matches 8; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 PNHF--RPAGLPEK 12  
I:|I |I|I |  
Db 698 PHFQGRPGAPRR 711

RESULT 12  
US-08-672-345C-3  
; Sequence 3, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 109 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-672-345C-3

Query Match 50.6%; Score 39; DB 2; Length 109;  
Best Local Similarity 41.7%; Pred. No. 24;  
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 NHFRPAGLPEKY 13  
I:|I |I|I |  
Db 52 NNYRPPGVPARF 63

RESULT 13  
US-08-672-345C-93  
; Sequence 93, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 93:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 109 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-672-345C-93

Query Match 50.6%; Score 39; DB 2; Length 109;  
Best Local Similarity 41.7%; Pred. No. 24;  
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 NHFRPAGLPEKY 13  
I:|I |I|I |  
Db 52 NNYRPPGVPARF 63

RESULT 14  
US-09-214-095D-3  
; Sequence 3, Application US/09214095D  
; Patent No. 6280987  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 51400-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/214,095D  
; CURRENT FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Murinae gen. Sp.  
US-09-214-095D-3

Query Match 50.6%; Score 39; DB 3; Length 109;  
Best Local Similarity 41.7%; Pred. No. 24;  
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 NHFRPAGLPEKY 13  
I:|I |I|I |  
Db 52 NNYRPPGVPARF 63

RESULT 15  
US-09-214-095D-121  
; Sequence 121, Application US/09214095D  
; Patent No. 6280987  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 51400-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/214,095D  
; CURRENT FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 121  
; LENGTH: 109  
; TYPE: PRT



; ORGANISM: Murine  
US-09-214-095D-121

Query Match 50.6%; Score 39; DB 3; Length 109;  
Best Local Similarity 41.7%; Pred. No. 24;  
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy 2 NHFRPAGLPKEY 13  
|::|||::|  
Db 52 NNYRPGVPARF 63

Search completed: August 18, 2003, 01:28:09  
Job time : 43 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 18, 2003, 01:15:09 ; Search time 43 seconds  
(without alignments)  
29.074 Million cell updates/sec

Title: US-09-846-779-1

Perfect score: 77

Sequence: 1 PNHRPAGLPEKY 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_76.\*

1: Pirl.\*

2: Pirl.\*

3: Pirl.\*

4: Pirl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	122	1 YLHUS	serum amyloid A1 p
2	77	100.0	122	1 YLHUA	serum amyloid A2 p
3	77	100.0	122	2 I39456	serum amyloid A2-b
4	77	100.0	122	4 JN0029	serum amyloid A3 p
5	74	96.1	116	2 D38645	amyloid A protein
6	74	96.1	116	2 D38645	amyloid A protein
7	74	96.1	119	1 YLDGA	amyloid protein AA
8	74	96.1	121	2 C38645	amyloid A protein
9	72	93.5	122	2 A35660	serum amyloid-rela
10	71	92.2	83	2 I71951	serum amyloid A -
11	71	92.2	129	2 B36451	serum amyloid A2 p
12	70	90.9	91	2 I71950	serum amyloid A -
13	70	90.9	122	2 A23521	serum amyloid A3 p
14	69	89.6	103	2 S06386	serum amyloid A pr
15	69	89.6	122	2 S32574	serum amyloid prot
16	69	89.6	122	2 JS0608	serum amyloid A pr
17	69	89.6	122	2 I46981	serum amyloid prot
18	69	89.6	122	2 I46982	serum amyloid prot
19	69	89.6	129	2 A36451	serum amyloid A1 p
20	68	88.3	110	2 A28573	serum amyloid A pr
21	68	88.3	130	2 A53167	serum amyloid A pr
22	67	87.0	122	2 A30248	serum amyloid AA-3
23	60	77.9	122	2 A23843	serum amyloid prot
24	60	77.9	122	2 I49496	amyloid A - mouse
25	58	75.3	122	2 B30248	serum amyloid AA1
26	58	75.3	122	2 C30248	serum amyloid AA2
27	57	74.0	122	2 B23843	serum amyloid prot
28	54	70.1	130	1 A38974	serum amyloid A4 p
29	46	59.7	404	2 T48098	hypothetical prote

## ALIGNMENTS

### RESULT 1

YLHUS  
serum amyloid A1 protein precursor [validated] - human  
N:Alternate names: amyloid-related serum protein SAA  
N:Contains: amyloid protein AA  
C:Species: Homo sapiens (man)  
C:Date: 15-Oct-1982 #sequence revision 08-Feb-1996 #text-change 08-Dec-2000  
C:Accession: A22342; S09972; S09974; S09977; S09978; S12491; S12492; S20103; A60863; 3196  
R:Siipe, J.D.; Colten, H.R.; Goldberger, G.; Edge, M.D.; Tack, B.F.; Cohen, A.S.; Whit  
Biochemistry 24, 2931-2936, 1985  
A:Title: Human serum amyloid A (SAA): biosynthesis and postsynthetic processing of p  
A:Reference number: A22342; MOID:85252712; PMID:3839415  
A:Contents: allele SAA1\*1 (SAA1-alpha)  
A:Accession: A22342  
A:Molecule type: mRNA  
A:Residues: 1-118, 'S', 120-122 <SIP>  
A:Cross-references: GB:M10906; NID:g337747; PIDN:AAA60297.1; PID:g337748  
R:Steinkasserer, A.; Weiss, E.H.; Schwaebler, W.; Linke, R.P.  
Biochem. J. 268, 187-193, 1990  
A:Title: Heterogeneity of human serum amyloid A protein: five different variants from  
A:Reference number: S09972; MOID:90262544; PMID:1971508  
A:Accession: S09972  
A:Molecule type: mRNA  
A:Residues: 8-72 <STE>  
A:Cross-references: EMBL:X51443  
A:Experimental source: clone PAS4  
A:Note: allele SAA1\*1 (SAA1-alpha)  
A:Accession: S09974  
A:Molecule type: mRNA  
A:Residues: 73-122 <ST2>  
A:Cross-references: EMBL:X51439; NID:g36311; PIDN:CAA35804.1; PID:g825714  
A:Experimental source: clone PAS1  
A:Note: allele SAA1\*1 (SAA1-alpha)  
A:Accession: S09977  
A:Molecule type: mRNA  
A:Residues: 73-74, 'V', 76-77, 'N', 79-122 <ST3>  
A:Cross-references: EMBL:X51442; NID:g36314; PIDN:CAA35807.1; PID:g825717  
A:Experimental source: clone PAS3-beta  
A:Note: a variant of allele SAA1-beta  
A:Accession: S09978  
A:Molecule type: mRNA  
A:Residues: 73-77, 'N', 79-122 <ST4>  
A:Cross-references: EMBL:X51441  
A:Experimental source: clone PAS3-alpha  
R:Linke, R.P.  
submitted to the EMBL Data Library, January 1990  
A:Reference number: S12491  
A:Accession: S12491  
A:Molecule type: mRNA  
A:Residues: 8-69, 'LG', <LIN>  
A:Cross-references: EMBL:X51443; NID:g36315; PIDN:CAA35808.1; PID:g939926

hypothetical prote  
ovarian tumor prot  
Ig lambda chain V  
collagen alpha 1(I  
hypothetical prote  
protein B0272.5 [i  
hypothetical prote  
amyloid protein A  
chelated iron tran  
sugar ABC transpor  
collagen alpha 1(I  
B-cell protein 8Hs  
Ig lambda chain V-  
phosphotransferase  
PTS system, IIA B c  
transposase homolo

30 46 59.7 1305 2 T23314  
31 45 58.4 88 2 B41760  
32 45 58.4 113 2 E44151  
33 45 58.4 921 2 S42617  
34 45 58.4 1555 2 T18688  
35 45 58.4 1373 2 G89608  
36 45 58.4 1973 2 T18686  
37 44 57.1 106 2 A27227  
38 44 57.1 297 2 AC0298  
39 44 57.1 364 2 H82727  
40 44 57.1 921 2 S40495  
41 42 54.5 123 2 S35302  
42 41 53.2 108 1 LSHUDL  
43 41 53.2 145 2 D81955  
44 41 53.2 152 2 B81013  
45 41 53.2 413 2 T31051

A:Experimental source: clone pAS4  
A:Note: allele SAAL\*1 (SAAL-alpha)  
A:Accession: S12492  
A:Molecule type: mRNA  
A:Residues: 73-74,'V',76-77,'N',79-122 <LI2>  
A:CROSS-references: EMBL:X51441; NID:G36313; PIDN:CAA35806.1; PID:9825716  
A:Experimental source: clone pAS3-alpha  
R:Betts, J.C.; Edbrooke, M.R.; Thakker, R.V.; Woo, P.  
Scand. J. Immunol. 34, 471-482, 1991  
A:Title: The human acute-phase serum amyloid A gene family: structure, evolution and expression  
A:Reference number: S20103; MUID:92022342; PMID:1636519  
A:Contents: allele SAAL\*2b (SAAL-beta)  
A:Accession: S20103  
A>Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-69,'A',71-74,'V',76-122 <BE2>  
A:CROSS-references: EMBL:X5652; NID:G36307; PIDN:CAA39974.1; PID:936308  
R:Skinner, M.; Pinnette, A.; Travis, W.D.; Shwachman, H.; Cohen, A.S.  
J. Lab. Clin. Med. 112, 413-417, 1988  
A:Title: Isolation and sequence analysis of amyloid protein AA from a patient with cysts  
Reference number: A60863; MUID:89010280; PMID:3171350  
A:Contents: allele SAAL\*1 (SAAL-alpha)  
A:Accession: A60863  
A:Molecule type: protein  
A:Residues: 19-94 <SKI>  
R:Parmelee, D.C.; Tifani, K.; Ericsson, L.H.; Eriksen, N.; Benditt, E.P.; Walsh, K.A.  
Biochemistry 21, 3298-3303, 1982  
A:Title: Amino acid sequence of amyloid-related apoprotein (apoSAA-1) from human high-density lipoprotein  
A:Reference number: A90461; MUID:83000248; PMID:71115671  
A:Contents: allele SAAL\*1 (SAAL-alpha)  
A:Accession: A90461  
A:Molecule type: protein  
A:Residues: 19-122 <PAR>  
A:Note: 70-Ala and 75-Val were also found  
A:Note: this protein was isolated from the high-density lipoprotein fraction of serum  
R:Sletten, K.; Marhaug, G.; Husby, G.  
Hoppe-Seyler's Z. Physiol. Chem. 364, 1039-1046, 1983  
A:Title: The covalent structure of amyloid-related serum protein SAA from two patients with amyloidosis  
A:Reference number: A91711; MUID:84030495; PMID:6629328  
A:Contents: allele SAAL\*1 (SAAL-alpha)  
A:Accession: A91711  
A:Molecule type: protein  
A:Residues: 19-40,'N',42-77,'N',79-92,'N',94-122 <SLE>  
A:Note: at least three polymorphic forms of this protein have been found in a patient with leucine are found at position 76  
R:Prelli, F.; Pras, M.; Frangione, B.  
Biochemistry 26, 8251-8256, 1987  
A:Title: Degradation and deposition of amyloid AA fibrils are tissue specific.  
Reference number: A29419; MUID:88163487; PMID:3442653  
A:Contents: allele SAAL\*1 (SAAL-alpha)  
A:Accession: A29419  
A:Molecule type: protein  
A:Residues: 20-100 <PRE>  
R:Westermarck, G.T.; Sletten, K.; Westermarck, P.  
Scand. J. Immunol. 30, 605-613, 1989  
A:Title: Massive vascular AA-amyloidosis: a histologically and biochemically distinctive entity  
A:Reference number: A60431; MUID:90069444; PMID:2587936  
A:Contents: allele SAAL\*1 (SAAL-alpha)  
A:Accession: A60431  
A:Molecule type: protein  
A:Residues: 19-98,'XXX',103-105,'X',107 <WES>  
R:Beauch, C.M.; de Beer, M.C.; Sipe, J.D.; Loose, L.D.; de Beer, F.C.  
Biochem. J. 282, 615-620, 1992  
A:Title: Human serum amyloid A protein. Complete amino acid sequence of a new variant.  
A:Reference number: S21260; MUID:92189607; PMID:1546977  
A:Contents: allele SAAL\*2a (SAAL-beta)  
A:Accession: S21261  
A:Molecule type: protein  
A:Residues: 18-69,'A',71-74,'V',76-89,'D',91-122 <BEA>  
A:Accession: S21260  
A:Molecule type: protein  
A:Residues: 20-69,'A',71-74,'V',76-89,'D',91-122 <BE2>  
R:Baba, S.; Takahashi, T.; Kasama, T.; Fujie, M.; Shirasawa, H.

Arch. Biochem. Biophys. 303, 361-366, 1993  
A:Title: A novel polymorphism of human serum amyloid A protein, SAA1gamma, is characterized by a single nucleotide substitution (G to A) at position 112 (G112A) in the coding region  
A:Reference number: S33864; MUID:93290347; PMID:8512321  
A:Contents: allele SAAL-gamma  
A:Accession: S33864  
A:Molecule type: protein  
A:Residues: 19-69,'A',71-122 <BAB>  
R:Baba, S.; Takahashi, T.; Kasama, T.; Shirasawa, H.  
Biochem. Biophys. Acta 1180, 195-200, 1992  
A:Title: Identification of two novel amyloid A protein subsets coexisting in an individual  
A:Reference number: A56867; MUID:93099171; PMID:1463770  
A:Contents: allele SAAL-gamma (allele 52,57-Ala)  
A:Accession: A56867  
A:Molecule type: protein  
A:Residues: 65-69,'A',71-80 <BA2>  
A:Experimental source: amyloid fibrils, thyroid gland of rheumatoid arthritis patient  
A:Note: sequence extracted from NCBI database (NCBI:121042)  
R:Moynier, K.; Sletten, K.; Husby, G.; Natvig, J.B.  
Scand. J. Immunol. 11, 549-554, 1980  
A:Title: An unusually large (83 amino acid residues) amyloid fibril protein AA from a patient with systemic amyloidosis  
A:Reference number: A94234; MUID:80213686; PMID:6155694  
A:Contents: Bol  
A:Accession: A94234  
A:Molecule type: protein  
A:Residues: 19-40,'N',42-83,'E',85-92,'N',94-95,'SEATVK' <MOY>  
A:Note: 70-Ala and 71-Arg were also found  
A:Note: this protein is from a patient with Waldenstrom's macroglobulinemia  
R:Sletten, K.; Husby, G.  
Eur. J. Biochem. 41, 117-125, 1974  
A:Title: The complete amino-acid sequence of non-immunoglobulin amyloid fibril protein  
A:Reference number: A91215; MUID:74120351; PMID:4816450  
A:Contents: Th  
A:Accession: A91215  
A:Molecule type: protein  
A:Residues: 19-40,'N',42-92,'N',94 <SL2>  
A:Note: this protein is from a patient with juvenile rheumatoid arthritis  
R:Sletten, K.; Husby, G.; Natvig, J.B.  
Biochem. Biophys. Res. Commun. 69, 19-25, 1976  
A:Title: The complete amino acid sequence of an amyloid fibril protein AA of unusual type  
A:Reference number: A90195; MUID:76160745; PMID:1259755  
A:Contents: J1  
A:Accession: A90195  
A:Molecule type: protein  
A:Residues: 19-40,'N',42-77,'N',79-82 <SL2>  
A:Note: 19-Arg is missing from some of the molecules  
A:Note: this protein is from a patient with ankylosing spondylitis  
R:Gorevic, P.D.; Prelli, F.C.; Wright, J.; Pras, M.; Frangione, B.  
J. Clin. Invest. 83, 836-843, 1989  
A:Title: Systemic senile amyloidosis. Identification of a new prealbumin (transferrin)opathy  
A:Reference number: A30323; MUID:89155805; PMID:2646319  
A:Accession: A30323  
A:Molecule type: protein  
A:Residues: 19-29 <GOR>  
R:Ullmar, C.M.; Burgess, C.J.; Sharp, P.M.; Whitehead, A.S.  
Genomics 19, 228-235, 1994  
A:Title: Evolution of the serum amyloid A (SAA) protein superfamily.  
A:Reference number: A38975; MUID:94245191; PMID:8188253  
A:Contents: annotation  
R:Kluve-Beckerman, B.; Dwyer, F.E.; Benson, M.D.  
J. Clin. Invest. 82, 1670-1675, 1988  
A:Title: Human serum amyloid A: three hepatic mRNAs and the corresponding proteins in liver  
A:Reference number: I39454; MUID:89034862; PMID:3183061  
A:Accession: I39454  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-122 <RES>  
A:CROSS-references: GB:M23698; NID:9758678; PIDN:AAA64799.1; PID:9758679  
C:Genetics: SAA  
A:Gene: GDB:SAA1; SAA  
A:CROSS-references: GDB:120364; OMIM:104750  
A:Map position: 11p15.1-11p15.1  
A:Introns: 31/1; 77/2

C:Superfamily: amyloid protein  
C:Keywords: acute phase; amyloid; HDL; polymorphism  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-122/Product: (or 20-122) serum amyloid A1 protein #status experimental <AP3>  
F:19-94/Product: (or 20-94) amyloid protein A1 #status experimental <AP3>  
  
Query Match 100.0%; Score 77; DB 1; Length 122;  
Best Local Similarity 100.0%; Pred. No. 6e-06; Gaps 0;  
Matches 13; Conservative 0; Mismatches 0; Indels 0;  
  
Qy 1 PNHRPAGLPEKY 13  
Db 110 PNHRPAGLPEKY 122  
  
RESULT 2  
YLHUA  
serum amyloid A2 protein precursor [validated] - human  
N:Alternate names: amyloid IV; amyloid protein AA (FMF); amyloid-related serum protein S  
;Species: Homo sapiens (man)  
;Date: 24-Apr-1984 #sequence\_revision 08-Feb-1996 #text\_change 08-Dec-2000  
C:Accession: A27902; S20104; S09975; S09976; S09973; B38974; A28445; A92763; A92112; A91  
R:Kluve-Beckerman, B.; Long, G.L.; Benson, M.D.  
Biochem. Genet. 24, 795-803, 1986  
A:Title: DNA sequence evidence for polymorphic forms of human serum amyloid A (SAA).  
A:Reference number: A27902; MUID:87095785; PMID:3800965  
A:Contents: allele SAA2\*1 (SAA2-alpha)  
A:Accession: A27902  
A:Molecule type: mRNA  
A:Residues: 1-122 <KLU>  
A:CROSS-references: GB:M26152; NID:g1160968; PIDN:AAA5338.1; PID:g1160969  
R:Betts, J.C.; Edbrooke, M.R.; Thakker, R.V.; Woo, P.  
Scand. J. Immunol. 34, 471-482, 1991  
A:Title: The human acute-phase serum amyloid A gene family: structure, evolution and exp  
A:Reference number: S20103; MUID:92022342; PMID:1656519  
A:Contents: allele SAA2\*1 (SAA2-alpha)  
A:Accession: S20104  
A:Molecule type: DNA  
A:Status: translation not shown  
A:Residues: 32-122 <BET>  
A:CROSS-references: EMBL:X56653; NID:g36309; PIDN:CAA39975.1; PID:g36310  
R:Steinkasserer, A.; Weiss, E.H.; Schwaebel, W.; Linke, R.P.  
Biochem. J. 268, 187-193, 1990  
A:Title: Heterogeneity of human serum amyloid A protein: five different variants from on  
A:Reference number: S09972; MUID:90262544; PMID:1971508  
A:Accession: S09975  
A:Molecule type: mRNA  
A:Residues: 1-55 <STE>  
A:CROSS-references: EMBL:X51444; NID:g36316; PIDN:CAA35809.1; PID:g36317  
A:Note: allele SAA2\*1 (SAA2-alpha)  
A:Accession: S09976  
A:Molecule type: mRNA  
A:Residues: 4-122 <ST2>  
A:CROSS-references: EMBL:X51445; NID:g36320; PIDN:CAA35810.1; PID:g36321  
A:Experimental source: clone pAS8  
A:Note: allele SAA2\*1 (SAA2-alpha)  
A:Accession: S09973  
A:Molecule type: mRNA  
A:Residues: 75-88, 'R', 90-122 <ST3>  
A:CROSS-references: EMBL:X51440; NID:g36312; PIDN:CAA35805.1; PID:g825715  
A:Experimental source: clone pAS2  
A:Note: allele SAA2\*2 (SAA2-beta)  
R:Steel, D.M.; Sellar, G.C.; Uhlar, C.M.; Simon, S.; DeBeer, F.C.; Whitehead, A.S.  
Genomics 16, 447-454, 1993  
A:Title: A constitutively expressed serum amyloid A protein gene (SAA4) is closely linke  
A:Reference number: A38974; MUID:93300520; PMID:7686132  
A:Contents: allele SAA2\*2 (SAA2-beta)  
A:Accession: B38974  
A:Molecule type: DNA  
A:Residues: 1-88, 'R', 90-122 <ST4>  
A:CROSS-references: GB:L05921  
R:Woo, P.; Sipe, J.; Dinarello, C.A.; Colten, H.R.

J. Biol. Chem. 262, 15790-15795, 1987  
A:Title: Structure of a human serum amyloid A gene and modulation of its expression  
A:Reference number: A28445; MUID:88058926; PMID:2890635  
A:Contents: allele SAA2\*2 (SAA2-beta)  
A:Accession: A28445  
A:Molecule type: DNA  
A:Residues: 1-14, 'G', 16-88, 'R', 90-122 <WOO>  
A:CROSS-references: GB:J03474; NID:g337742; PIDN:AAB59539.1; PID:g337743  
R:Levin, M.; Franklin, E.C.; Frangione, B.; Pras, M.  
J. Clin. Invest. 51, 2773-2776, 1972  
A:Title: The amino acid sequence of a major nonimmunoglobulin component of some amyl.  
A:Reference number: A92763; MUID:72268653; PMID:5056669  
A:Contents: allele SAA2\*2 (SAA2-beta)  
A:Accession: A92763  
A:Molecule type: protein  
A:Residues: 19-70, 'R', 72-88, 'R', 90-94 <LEV>  
A:Note: this protein is from a patient with familial Mediterranean fever  
A:Note: the sequence of residues 19-72 of amyloid protein AA from a patient with tub.  
R:Ein, D.; Kinura, S.; Terry, W.D.; Magnotta, J.; Glenner, G.G.  
J. Biol. Chem. 247, 5653-5655, 1972  
A:Title: Amino acid sequence of an amyloid fibril protein of unknown origin.  
A:Reference number: A92112; MUID:72266694; PMID:5055786  
A:Accession: A92112  
A:Molecule type: protein  
A:Residues: 19-63 <EIN>  
A:Note: this amyloid IV was isolated from a patient with rheumatoid arthritis  
R:Benditt, E.P.; Eriksen, N.; Hermanson, M.A.; Ericsson, L.H.  
FEBS Lett. 19, 169-173, 1971  
A:Title: The major proteins of human and monkey amyloid substance: common properties  
A:Reference number: A91345  
A:Accession: A91345  
A:Molecule type: protein  
A:Residues: 19-42 <BEN>  
A:Note: the amino-terminal tripeptide is sometimes missing  
A:Note: this protein is from a patient with generalized amyloidosis associated with  
R:Baba, S.; Takahashi, T.; Kasama, T.; Shirasawa, H.  
Biochim. Biophys. Acta 1180, 195-200, 1992  
A:Title: Identification of two novel amyloid A protein subsets coexisting in an indi  
A:Reference number: A56867; MUID:93099171; PMID:1463770  
A:Contents: allele SAA2\*1 (SAA2-alpha)  
A:Accession: B56867  
A:Molecule type: protein  
A:Residues: 65-80 <BAB>  
A:Experimental source: amyloid fibrils, thyroid gland of rheumatoid arthritis patient  
A:Note: sequence extracted from NCBI backbone (NCBIP:121046)  
R:Kluve-Beckerman, B.; Dwulet, F.E.; Benson, M.D.  
J. Clin. Invest. 82, 1670-1675, 1988  
A:Title: Human serum amyloid A. Three hepatic mRNAs and the corresponding proteins i  
A:Reference number: I39454; MUID:89034862; PMID:3183061  
A:Accession: I39455  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-122 <RES>  
A:CROSS-references: GB:M23699; NID:g758680; PIDN:AAA64800.1; PID:g758681  
C:Genetics:  
A:Gene: GDB:SAA2  
A:CROSS-references: GDB:132592; OMIM:104751  
A:Map position: 11p15.1-11p15.1  
A:Introns: 31/1; 77/2  
C:Superfamily: amyloid protein  
C:Keywords: acute phase; amyloid; polymorphism  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-94/Product: serum amyloid A2 protein #status experimental <MAT>  
  
Query Match 100.0%; Score 77; DB 1; Length 122;  
Best Local Similarity 100.0%; Pred. No. 6e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 PNHRPAGLPEKY 13  
Db 110 PNHRPAGLPEKY 122

```
RESULT 3
139456
serum amyloid A2-beta - human
C:Species: Homo sapiens (man)
C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 20-Aug-1999
A:Reference number: 139456
C:Accession: J39456
R:Kluwe-Beckerman, B.; Dwulet, F.E.; Benson, M.D.
J. Clin. Invest. 82, 1670-1675, 1988
A:Title: Human serum amyloid A. Three hepatic mRNAs and the corresponding proteins in on
A:Reference number: 139454; MUID:89034862; PMID:3183061
A:Accession: J39456
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-122 <RES>
A:CROSS-references: GB:M23700; NID:g758682; PIDN:AAA64801.1; PTD:g758683
C:Genetics:
A:Gene: GDB:SAA2
A:CROSS-references: GDB:132592; OMIM:104751
A:Map position: lip15.1-1p15.1
A:Superfamily: amyloid protein

Query Match 100.0%; Score 77; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNHRFPAGLPEKY 13
DB 110 PNHRFPAGLPEKY 122

RESULT 4
JN0029
serum amyloid A3 pseudogene - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 17-May-1996 #text_change 20-Apr-2000
C:Accession: JN0029
R:Sack Jr., G.H.; Talbot Jr., C.C.
Gene 84, 509-515, 1989
A:Title: The human serum amyloid A (SAA)-encoding gene GSAA1: nucleotide sequence and po
A:Reference number: JN0029
A:Accession: JN0029
A:Status: conceptual translation of pseudogene
A:Molecule type: DNA
A:Residues: 1-122 <SAC>
A:CROSS-references: EMBL:X13895; NID:g36305; PIDN:CNA32096.1; PTD:g36306
R:Steel, D.M.; Sellar, G.C.; Uhlar, C.M.; Simon, S.; DeBeer, F.C.; Whitehead, A.S.
Genomics 16, 447-454, 1993
A:Title: A constitutively expressed serum amyloid A protein gene (SAA4) is closely linke
Reference number: A38974; MUID:93300520; PMID:7686132
Contents: annotation
A:Note: references cited confirm a frameshift error between codons 30 and 32 that leads
C:Genetics:
A:Gene: GDB:SAA3; GSAA1
A:CROSS-references: GDB:132593
A:Map position: lip15.1-p14
A:Introns: 31/1; 77/2
C:Keywords: pseudogene

Query Match 100.0%; Score 77; DB 4; Length 122;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNHRFPAGLPEKY 13
DB 110 PNHRFPAGLPEKY 122

RESULT 5
D38645
amyloid A protein DSAA85 precursor - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change 20-Aug-1999
C:Accession: D38645
R:Kluwe-Beckerman, B.; Dwulet, F.E.; DiBartola, S.P.; Benson, M.D.
Comp. Biochem. Physiol. B 94, 175-183, 1989
A:Title: Primary structures of dog and cat amyloid A proteins: comparison to human AA
A:Reference number: JLO110; MUID:90091422; PMID:2598632
A:Accession: JLO110
A:Molecule type: protein
A:Residues: 9-101 <KLU>
A:Note: 25-Trp was also found
C:Comment: This protein is the main constituent of reactive amyloid fibrils in man an
C:Comment: The extracellular deposits formed by this protein are highly insoluble and
C:Superfamily: amyloid protein
C:Keywords: amyloid; pyroglutamic acid

R:Sellar, G.C.; DeBeer, M.C.; Lelias, J.M.; Snyder, P.W.; Glickman, L.T.; Felsburg, P
J. Biol. Chem. 266, 3505-3510, 1991
A:Title: Dog serum amyloid A protein. Identification of multiple isoforms defined by
A:Reference number: A38645; MUID:91139635; PMID:1995613
A:Accession: D38645
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-116 <SEL>
A:CROSS-references: GB:M59174; NID:g164065; PIDN:AAA62765.1; PID:g164066
C:Superfamily: amyloid protein

Query Match 96.1%; Score 74; DB 2; Length 116;
Best Local Similarity 92.3%; Pred. No. 1.9e-05;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNHRFPAGLPEKY 13
DB 104 PNHRFPAGLPEKY 116

RESULT 6
E38645
amyloid A protein DSAA86 precursor - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change 20-Aug-1999
C:Accession: E38645
R:Sellar, G.C.; DeBeer, M.C.; Lelias, J.M.; Snyder, P.W.; Glickman, L.T.; Felsburg, P
J. Biol. Chem. 266, 3505-3510, 1991
A:Title: Dog serum amyloid A protein. Identification of multiple isoforms defined by
A:Reference number: A38645; MUID:91139635; PMID:1995613
A:Accession: E38645
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-116 <SEL>
A:CROSS-references: GB:M59175; NID:g164067; PIDN:AAA51457.1; PID:g164068
C:Superfamily: amyloid protein

Query Match 96.1%; Score 74; DB 2; Length 116;
Best Local Similarity 92.3%; Pred. No. 1.9e-05;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNHRFPAGLPEKY 13
DB 104 PNHRFPAGLPEKY 116

RESULT 7
YLDGA
amyloid protein AA precursor (clone DSAA15) - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 30-Sep-1990 #sequence_revision 12-Apr-1996 #text_change 11-May-2000
C:Accession: A38645; JLO110
R:Sellar, G.C.; DeBeer, M.C.; Lelias, J.M.; Snyder, P.W.; Glickman, L.T.; Felsburg, P
J. Biol. Chem. 266, 3505-3510, 1991
A:Title: Dog serum amyloid A protein. Identification of multiple isoforms defined by
A:Reference number: A38645; MUID:91139635; PMID:1995613
A:Accession: A38645
A:Molecule type: mRNA
A:Residues: 1-119 <SEL>
A:CROSS-references: GB:M59171; NID:g164059; PIDN:AAA62762.1; PID:g164060
R:Kluwe-Beckerman, B.; Dwulet, F.E.; DiBartola, S.P.; Benson, M.D.
Comp. Biochem. Physiol. B 94, 175-183, 1989
A:Title: Primary structures of dog and cat amyloid A proteins: comparison to human AA
A:Reference number: JLO110; MUID:90091422; PMID:2598632
A:Accession: JLO110
A:Molecule type: protein
A:Residues: 9-101 <KLU>
A:Note: 25-Trp was also found
C:Comment: This protein is the main constituent of reactive amyloid fibrils in man an
C:Comment: The extracellular deposits formed by this protein are highly insoluble and
C:Superfamily: amyloid protein
C:Keywords: amyloid; pyroglutamic acid
```

F;1-8/Domain: signal sequence (fragment) #status predicted <SIG>  
F;9-10/Product: amyloid protein AA #status experimental <MAT>  
F;9/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment

Query Match 96.1%; Score 74; DB 1; Length 119;  
Best Local Similarity 92.3%; Pred. No. 1.9e-05;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNHRPAGLPKPY 13  
|||||  
Db 107 PNHRPAGLPDKY 119

RESULT 8  
C38645  
amyloid A protein DSAA32 precursor - dog (fragment)  
C:Species: Canis lupus familiaris (dog)  
C:Date: 21-Feb-1992 #sequence\_revision 21-Feb-1992 #text\_change 20-Aug-1999  
C:Accession: C38645  
Sellar, G.C.; DeBeer, M.C.; Lelias, J.M.; Snyder, P.W.; Glickman, L.T.; Felsburg, P.J.  
Biol. Chem. 266, 3505-3510, 1991  
A:Title: Dog serum amyloid A protein. Identification of multiple isoforms defined by cDN  
A:Reference number: A38645; MUID:91139635; PMID:1995613  
A:Accession: C38645  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-121 <SEL>  
A:Cross-references: GB:M59173; NID:g164063; PIDN:AAA62764.1; PID:g164064  
C:Superfamily: amyloid protein

Query Match 96.1%; Score 74; DB 2; Length 121;  
Best Local Similarity 92.3%; Pred. No. 1.9e-05;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNHRPAGLPKPY 13  
|||||  
Db 109 PNHRPAGLPDKY 121

RESULT 9  
A35660  
serum amyloid-related protein SAA3 - hamster  
C:Species: Cricetinae gen. sp. (hamster)  
C:Date: 28-Sep-1990 #sequence\_revision 28-Sep-1990 #text\_change 20-Aug-1999  
R;Gervais, C.; Suh, M.  
Mol. Cell. Biol. 10, 4412-4414, 1990  
A:Title: Serum amyloid A protein-related mRNA expression in herpes simplex virus type 2-  
A:Reference number: A35660; MUID:90318412; PMID:2164641  
A:Accession: A35660  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-122 <GER>  
A:Cross-references: GB:M33431; NID:g191440; PIDN:AAA37098.1; PID:g305362  
C:Superfamily: amyloid protein

Query Match 93.5%; Score 72; DB 2; Length 122;  
Best Local Similarity 92.3%; Pred. No. 4.3e-05;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PNHRPAGLPKPY 13  
|||||  
Db 110 PNHRPAGLPKPY 122

RESULT 10  
I71951  
serum amyloid A - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 20-Aug-1999  
C:Accession: I71951  
R;Yamamoto, K.  
J. Immunol. 139, 1683-1688, 1987

A:Title: Structural diversity of murine serum amyloid A genes: Evolutionary implicat  
A:Reference number: I55984; MUID:87309776; PMID:3624868  
A:Accession: I71951  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-83 <RES>  
A:Cross-references: GB:M17790; NID:g200920; PIDN:AAA40089.1; PID:g200921  
C:Genetics:  
A:Introns: 38/2  
C:Superfamily: amyloid protein

Query Match 92.2%; Score 71; DB 2; Length 83;  
Best Local Similarity 84.6%; Pred. No. 4.4e-05;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNHRPAGLPKPY 13  
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Db 71 PNHRPAGLPDKY 83

RESULT 11  
B36451  
serum amyloid A2 precursor - American mink  
C:Species: Mustela vison (American mink)  
C:Date: 08-Mar-1991 #sequence\_revision 08-Mar-1991 #text\_change 20-Aug-1999  
C:Accession: B36451  
R;Marhaug, G.; Husby, G.; Dowton, S.B.  
J. Biol. Chem. 265, 10049-10054, 1990  
A:Title: Mink serum amyloid A protein. Expression and primary structure based on cDN  
A:Reference number: A36451; MUID:90277614; PMID:2351648  
A:Accession: B36451  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-129 <MAR>  
A:Cross-references: GB:M34954; GB:J05445; NID:g164267; PIDN:AAA30969.1; PID:g164268  
C:Superfamily: amyloid protein

Query Match 92.2%; Score 71; DB 2; Length 129;  
Best Local Similarity 84.6%; Pred. No. 6.8e-05;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNHRPAGLPKPY 13  
|||||  
Db 117 PNHRPAGLPDKY 129

RESULT 12  
I71950  
serum amyloid A - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 20-Aug-1999  
C:Accession: I71950  
R;Yamamoto, K.  
J. Immunol. 139, 1683-1688, 1987  
A:Title: Structural diversity of murine serum amyloid A genes: Evolutionary implicat  
A:Reference number: I55984; MUID:87309776; PMID:3624868  
A:Accession: I71950  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-91 <RES>  
A:Cross-references: GB:M17792; NID:g200917; PIDN:AAA40088.1; PID:g200919  
C:Genetics:  
A:Introns: 46/2  
C:Superfamily: amyloid protein

Query Match 90.9%; Score 70; DB 2; Length 91;  
Best Local Similarity 84.6%; Pred. No. 7.1e-05;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNHRPAGLPKPY 13  
|||||  
Db 79 PNHRPAGLPKPY 91

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RESULT 13
A23521
serum amyloid A3 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 20-Aug-1999
C:Accession: A23521; B23521; C23843; I49495
R:Stearman, R.S.; Lowell, C.A.; Peltzman, C.G.; Morrow, J.F.
Nucleic Acids Res. 14, 797-809, 1986
A:Title: The sequence and structure of a new serum amyloid A gene.
A:Reference number: A23521; MUID:86120372; PMID:3003697
A:Accession: A23521
A:Molecule type: DNA
A:Residues: 1-30 <ST1>
A:Accession: B23521
A:Molecule type: mRNA
A:Residues: 27-122 <ST2>
A:CROSS-references: GB:X03479; NID:954035; PIDN:CAA27199.1; PID:g817998
R:Lowell, C.A.; Potter, D.A.; Stearman, R.S.; Morrow, J.F.
  Biol. Chem. 261, 8442-8452, 1986
  Title: Structure of the murine serum amyloid A gene family. Gene conversion.
  Reference number: A23843; MUID:86250747; PMID:3013853
A:Accession: C23843
A:Molecule type: DNA
A:Residues: 1-122 <LOW>
R:Stearman, R.S.; Lowell, C.A.; Pearson, W.R.; Morrow, J.F.
Ann. N. Y. Acad. Sci. 389, 106-115, 1982
A:Title: Regulation of synthesis of amyloid A-related protein.
A:Reference number: I49495; MUID:82229376; PMID:6953913
A:Accession: I49495
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 27-64 <RES>
A:CROSS-references: GB:M25467; NID:gl91929; PIDN:AAA37231.1; PID:gl91930
C:Genetics:
A:introns: 31/1; 77/2
C:Superfamily: amyloid protein
C:Keywords: acute phase; amyloid
F:19-122/Product: serum amyloid-related protein SAA3 #status predicted <MAT>

Query Match      90.9%; Score 70; DB 2; Length 122;
Best Local Similarity 84.6%; Pred. No. 9.5e-05;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 PNHFRPAGLPKY 13
        ||||| |||:|
DB      110 PNHFRPAGLPKY 122

JULT 14
>06386
serum amyloid A protein precursor - American mink
C:Species: Mustela vison (American mink)
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 05-Aug-1994
C:Accession: S06386
R:Syversen, V.; Sletten, K.; Marhaug, G.; Husby, G.; Liim, B.
Scand. J. Immunol. 26, 763-767, 1987
A:Title: The amino acid sequence of serum amyloid A (SAA) protein in mink.
A:Reference number: S06386; MUID:88099357; PMID:3423742
A:Accession: S06386
A:Molecule type: protein
A:Residues: 1-103 <STV>
A:Note: 10-Val, 67-Val, and 71-Phe were also found
C:Superfamily: amyloid protein
C:Keywords: amyloid; pyroglutamic acid
F:1-103/Product: amyloid protein A, serum #status experimental <MAT1>
F:1-64/Product: amyloid protein A, amyloid (long form) #status experimental <MAT2>
F:1-53/Product: amyloid protein A, amyloid (short form) #status experimental <MAT3>
F:1/Modified site: pyroglutamic acid (Gln) #status experimental

Query Match      89.6%; Score 69; DB 2; Length 103;
Best Local Similarity 84.6%; Pred. No. 0.00012;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 PNHFRPAGLPKY 13
        ||||| |||:|
DB      91 PNHFRPAGLPKY 103

RESULT 15
S32574
serum amyloid protein SAA - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
C:Accession: S32574
R:Mitchell, T.I.; Coop, C.I.; Brinckerhoff, C.E.
J. Clin. Invest. 87, 1177-1185, 1991
A:Title: Serum amyloid A (SAA3) produced by rabbit synovial fibroblasts treated with
A:Reference number: S32574; MUID:91185595; PMID:1849144
A:Accession: S32574
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-122 <MIT>
A:CROSS-references: EMBL:M64696; NID:gl65698; PIDN:AAA31464.1; PID:gl65699
C:Superfamily: amyloid protein

Query Match      89.6%; Score 69; DB 2; Length 122;
Best Local Similarity 84.6%; Pred. No. 0.00014;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 PNHFRPAGLPKY 13
        ||||| |||:|
DB      110 PNHFRPAGLPKY 122

Search completed: August 18, 2003, 01:27:14
Job time : 45 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 17, 2003, 23:55:27 ; Search time 37 Seconds  
(without alignments)  
16.523 Million cell updates/sec

Title: US-09-846-779-1  
Perfect score: 77  
Sequence: 1 PNHFRPAGLPEKY 13

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	77	100.0	122	1 SAA3_HUMAN	P22614 homo sapien
2	77	100.0	122	1 SAA3_HUMAN	P02735 homo sapien
3	74	96.1	112	1 SAA1_BOVIN	P35541 bos taurus
4	74	96.1	129	1 SAA1_CANFA	P19708 canis fami
5	72	93.5	122	1 SAA3_MESAU	P19453 mesocricetu
6	71	92.2	102	1 SAA5_MESAU	P81491 mesocricetu
7	71	92.2	129	1 SAA2_MUSVI	P02739 mustela vis
8	70	90.9	122	1 SAA3_MOUSE	P04918 mus musculu
9	69	89.6	112	1 SAA1_SHEEP	P42819 ovis aries
10	69	89.6	122	1 SAA1_RABIT	P33614 oryctolagus
11	69	89.6	122	1 SAA2_RABIT	P22000 oryctolagus
12	69	89.6	122	1 SAA3_RABIT	P35543 oryctolagus
13	69	89.6	129	1 SAA1_MUSVI	P18575 mustela vis
14	68	88.3	110	1 SAA1_HORSE	P19857 equus cabal
15	68	88.3	130	1 SAA1_MOUSE	P31532 mus musculu
16	60	77.9	122	1 SAA1_MOUSE	P05366 mus musculu
17	58	75.3	122	1 SAA1_MESAU	P20726 mesocricetu
18	58	75.3	122	1 SAA1_MESAU	P20727 mesocricetu
19	57	74.0	122	1 SAA2_MOUSE	P05367 mus musculu
20	56	72.7	127	1 SAA1_ANAPL	P02740 anas platyr
21	54	70.1	130	1 SAA4_HUMAN	P35542 homo sapien
22	47	61.0	127	1 SAA4_MACEU	P33613 mactopus eu
23	44	57.1	297	1 YFED_YERPE	Q56955 versinia pe
24	44	57.1	921	1 CA13_MOUSE	Q05732 mus musculu
25	41	53.2	108	1 LV5A_HUMAN	P01719 homo sapien
26	41	53.2	646	1 YEG1_ECO57	Q8x738 escherichia
27	41	53.2	648	1 YEG1_ECOLI	P76393 escherichia
28	41	53.2	864	1 SBE2_YEAST	P42223 saccharomyc
29	40	51.9	412	1 KAPR_EMENI	O59922 americhella
30	40	51.9	676	1 KALM_CHICK	P33005 gallus gall
31	39	50.6	109	1 LV11_HUMAN	P06888 homo sapien
32	39	50.6	111	1 LV1D_HUMAN	P01702 homo sapien
33	39	50.6	123	1 VPR3_HUMAN	Q9uk13 homo sapien

ALIGNMENTS

RESULT 1  
SAA3\_HUMAN STANDARD; PRT; 122 AA.  
AC P22614; Q95735;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Putative serum amyloid A-3 protein.  
GN SAA3P OR SAA3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90128298; PubMed=2558975;  
RA Sack G.H. Jr., Talbot C.C. Jr.;  
RT "The human serum amyloid A (SAA)-encoding gene GSAA1: nucleotide  
RT sequence and possible autoocrine-collagenase-inducer function.";  
RL Gene 84:509-515(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92096115; PubMed=1755958;  
RA Kluev-Beckerman B., Drumm M.L., Benson M.D.;  
RT "Nonexpression of the human serum amyloid A three (SAA3) gene.";  
RL DNA Cell Biol. 10:651-661(1991).  
CC -!- SIMILARITY: BELONGS TO THE SAA FAMILY.  
CC -!- CAUTION: This is probably the product of a pseudogene.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/  
CC or send an email to license@isb-sib.ch).  
EMBL; X13895; CAA32096.1; ALT\_INIT.  
EMBL; S73444; .; NOT\_ANNOTATED\_CDS.  
PIR; JN0029; JN0029.  
Gene; HGNC:10515; SAA3P.  
InterPro; IPR000096; Serum\_amyloid\_A.  
Pfam; PF00277; SAA\_proteins; 1.  
PRINTS; PR00306; SERUMAMYLLOID.  
ProDom; PD002112; Serum\_amyloid\_A; 1.  
SMART; SM00197; SAA; 1.  
PROSITE; PS00992; SAA; 1.  
KW Hypothetical protein.  
FT CONFLICT 5 5 T -> Y (IN REF. 2).  
FT CONFLICT 32 32 A -> T (IN REF. 2).  
FT CONFLICT 37 37 R -> K (IN REF. 2).  
FT CONFLICT 49 49 K -> N (IN REF. 2).  
FT CONFLICT 57 57 R -> W (IN REF. 2).  
FT CONFLICT 67 69 PGK -> LGA (IN REF. 2).  
SEQUENCE 122 AA; 13440 MW; 70F0ECC052E08472 CRC64;

34 39 50.6 130 1 LV1G\_HUMAN P06316 homo sapien  
35 39 50.6 154 1 ELYS\_HALRU P04552 halloitis ru  
36 39 50.6 446 1 CLUS\_PIG Q29549 sus scrofa  
37 39 50.6 448 1 CLUS\_MOUSE Q06890 mus musculus  
38 39 50.6 520 1 JKRY\_HUMAN O75364 homo sapien  
39 39 50.6 557 1 JKRY\_MOUSE Q60976 mus musculus  
40 39 50.6 680 1 DCML\_HUMAN P23352 homo sapien  
41 39 50.6 809 1 DCML\_OLICA P19919 oligotropha  
42 39 50.6 2923 1 CLR2\_HUMAN Q9hcu4 homo sapien  
43 38 49.4 106 1 LV4A\_HUMAN P01715 homo sapien  
44 38 49.4 111 1 LV3B\_HUMAN P80748 homo sapien  
45 38 49.4 289 1 EIA\_ADE02 P03254 human adeno



Query Match 100.0%; Score 77; DB 1; Length 122;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-06;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PNHFRPAGLPEKY 13  
 |||||  
 DB 110 PNHFRPAGLPEKY 122

RESULT 2  
 SAA1\_HUMAN  
 ID SAA1\_HUMAN STANDARD; PRT; 122 AA.  
 AC P02735; P02736; P02737; Q16730; Q16835; Q16879; Q96QNO;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Serum amyloid A protein precursor (SAA) [Contains: Amyloid protein A  
 (Amyloid fibril protein AA)].  
 DE SAA1 AND SAA2.  
 GN Homo sapiens (Human).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 JC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 SEQUENCE FROM N.A.  
 RX MEDLINE=85252712; PubMed=3839415;  
 RA Sipe J.D., Colten H.R., Goldberger G., Edge M.D., Tack B.F.,  
 RA Cohen A.S., Whitehead A.S.;  
 RT "Human serum amyloid A (SAA): biosynthesis and postsynthetic  
 processing of preSAA and structural variants defined by complementary  
 DNA.";  
 RL Biochemistry 24:2931-2936(1985).  
 RN [2]  
 SEQUENCE FROM N.A.  
 RX MEDLINE=88058926; PubMed=2890635;  
 RA Woo P., Sipe J., Dinarello C.A., Colten H.R.;  
 RT "Structure of a human serum amyloid A gene and modulation of its  
 RT expression in transfected L cells.";  
 RL J. Biol. Chem. 262:15790-15795(1987).  
 RN [3]  
 SEQUENCE FROM N.A.  
 RX MEDLINE=87099785; PubMed=3800865;  
 RA Kluge-Beckerman B., Long G.L., Benson M.D.;  
 RT "DNA sequence evidence for polymorphic forms of human serum amyloid A  
 RT (SAA)." ;  
 RL Biochem. Genet. 24:795-803(1986).  
 RN [4]  
 SEQUENCE FROM N.A. (SAA1 AND SAA2).  
 RX TISSUP=Liver;  
 RA Kluge-Beckerman B., Dwulet F.E., Benson M.D.;  
 RT "Human serum amyloid A. Three hepatic mRNAs and the corresponding  
 RT proteins in one person." ;  
 RL J. Clin. Invest. 82:1670-1675(1988).  
 RN [5]  
 SEQUENCE FROM N.A.  
 RX TISSUP=Liver;  
 RA MEDLINE=90262544; PubMed=1971508;  
 RA Steinkasserer A., Weiss E.H., Schwaebel W., Linke R.P.;  
 RT "Heterogeneity of human serum amyloid A protein. Five different  
 RT variants from one individual demonstrated by cDNA sequence  
 RT analysis." ;  
 RL Biochem. J. 268:187-193(1990).  
 RN [6]  
 SEQUENCE FROM N.A. (SAA1 AND SAA2 ALPHA).  
 RX TISSUP=Liver;  
 RA MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Ingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences." ;  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [7]  
 SEQUENCE OF 19-122.  
 RX MEDLINE=8300248; PubMed=7115671;  
 RA Parmelee D.C., Titani K., Ericsson L.H., Eriksen N., Benditt E.P.,  
 RA Walsh K.A.;  
 RT "Amino acid sequence of amyloid-related apoprotein (apoSAA1) from  
 RT human high-density lipoprotein." ;  
 RL Biochemistry 21:3298-3303(1982).  
 RN [8]  
 SEQUENCE OF 19-122 (VARIANT 1-BETA).  
 RX MEDLINE=92189607; PubMed=1546977;  
 RA Beach C.M., de Beer M.C., Sipe J.D., Loose L.D., de Beer F.C.;  
 RT "Human serum amyloid A protein. Complete amino acid sequence of a new  
 RT variant." ;  
 RL Biochem. J. 282:615-620(1992).  
 RN [9]  
 SEQUENCE OF 20-100.  
 RX MEDLINE=88163487; PubMed=3442653;  
 RA Prelli F., Pras M., Frangione B.;  
 RT "Degradation and deposition of amyloid AA fibrils are tissue  
 RT specific." ;  
 RL Biochemistry 26:8251-8256(1987).  
 RN [10]  
 SEQUENCE OF 19-94 (FAMILIAL MEDITERRANEAN FEVER PATIENT).  
 RX MEDLINE=72268653; PubMed=5056669;  
 RA Levin M., Franklin E.C., Frangione B., Pras M.;  
 RT "The amino acid sequence of a major nonimmunoglobulin component of  
 RT some amyloid fibrils." ;  
 RL J. Clin. Invest. 51:2773-2776(1972).  
 RN [11]  
 SEQUENCE OF 19-94 (TUBERCULOSIS PATIENT).  
 RX MEDLINE=72266694; PubMed=5055786;  
 RA Ein D., Kimura S., Terry W.D., Magnotta J., Glennen G.G.;  
 RT "Amino acid sequence of an amyloid fibril protein of unknown origin." ;  
 RL J. Biol. Chem. 247:5653-5655(1972).  
 RN [12]  
 SEQUENCE OF 19-94 (TH).  
 RX MEDLINE=74120351; PubMed=4816450;  
 RA Sletten K., Husby G.;  
 RT "The complete amino-acid sequence of non-immunoglobulin amyloid  
 RT fibril protein AS in rheumatoid arthritis." ;  
 RL Eur. J. Biochem. 41:117-125(1974).  
 RN [13]  
 SEQUENCE OF 19-82 (JL).  
 RX MEDLINE=76160745; PubMed=1259755;  
 RA Sletten K., Husby G., Natvig J.B.;  
 RT "The complete amino acid sequence of an amyloid fibril protein AAL of  
 RT unusual size (64 residues)." ;  
 RL Biochem. Biophys. Res. Commun. 69:19-25(1976).  
 RN [14]  
 SEQUENCE OF 19-101 (BOL).  
 RX MEDLINE=80213686; PubMed=6155694;  
 RA Moynier K., Sletten K., Husby G., Natvig J.B.;  
 RT "An unusually large (83 amino acid residues) amyloid fibril protein  
 RT AA from a patient with Waldenstrom's macroglobulinaemia and  
 RT amyloidosis." ;  
 RL Scand. J. Immunol. 11:549-554(1980).  
 RN [15]  
 SEQUENCE OF 19-42.

RA Benditt E.P., Eriksen N., Hermodson M.A., Ericsson L.H.;  
RT "The major proteins of human and monkey amyloid substance: common  
RL properties including unusual N-terminal amino acid sequences.";  
RN FEBS Lett. 19:169-173(1971).  
RC [16]  
RP SEQUENCE OF 32-122 FROM N.A.  
RC TISSUE=LIVER;  
RA MEDLINE=93290347; PubMed=1656519;  
RX Baba S., Takahashi T., Kasama T., Fujie M., Shirasawa H.;  
RT "A novel polymorphism of human serum amyloid A protein, SAA1 gamma,  
RL is characterized by alanines at both residues 52 and 57.";  
RN Arch. Biochem. Biophys. 303:361-366(1993).  
RC [17]  
RP VARIANT 1-GAMMA.  
RX MEDLINE=93290347; PubMed=8512321;  
RA Baba S., Takahashi T., Kasama T., Fujie M., Shirasawa H.;  
RT "A novel polymorphism of human serum amyloid A protein, SAA1 gamma,  
RL is characterized by alanines at both residues 52 and 57.";  
RN Arch. Biochem. Biophys. 303:361-366(1993).  
RC [18]  
RP PARTIAL SEQUENCE (VARIOUS FORMS), AND METHYLATION OF ASN-101.  
RX MEDLINE=96377164; PubMed=8783012;  
RA Ducet A., Bruun C.F., Bures E.J., Marhaug G., Husby G.,  
RT Abersold R.;  
RL "Characterization of human serum amyloid A protein isoforms separated  
by two-dimensional electrophoresis by liquid  
chromatography/electrospray ionization tandem mass spectrometry.";  
RN Electrophoresis 17:866-876(1996).  
CC -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL  
COMPLEX.  
CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.  
CC -1- INDUCTION: UPON CYTOKINE STIMULATION.  
CC -1- PTM: THIS PROTEIN IS THE PRECURSOR OF AMYLOID PROTEIN A, WHICH IS  
FORMED BY THE REMOVAL OF APPROXIMATELY 24 RESIDUES FROM THE  
CARBOXYL END.  
CC -1- POLYMORPHISM: BOTH SAA1 AND SAA2 HAVE A NUMBER OF ALLELES. WE USE  
HERE THE NOMENCLATURE OF REF.6. THE SEQUENCE SHOWN IS THAT OF  
1-ALPHA.  
CC -1- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE  
EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.  
CC THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS;  
CC THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.  
CC -1- DISEASE: BOLL IS FROM A PATIENT WITH WALDENSTROM'S  
MACROGLOBULINEMIA.  
CC -1- DISEASE: JL IS FROM A PATIENT WITH ANKYLOSING SPONDYLITIS.  
CC -1- DISEASE: TH IS FROM A PATIENT WITH JUVENILE RHEUMATOID ARTHRITIS.  
CC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.  
CC -----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; M10906; AAA60297.1; -  
DR EMBL; J03474; AAB59539.1; -  
DR EMBL; M23698; AAA64799.1; -  
DR EMBL; M23699; AAA64800.1; -  
DR EMBL; M23700; AAA64801.1; -  
DR EMBL; M26152; AAA85338.1; -  
DR EMBL; BC007022; AAH07022.1; -  
DR EMBL; BC020795; AAH20795.1; -  
DR EMBL; X51439; CAA35804.1; -  
Query Match 100.0%; Score 77; DB 1; Length 122;  
Best Local Similarity 100.0%; Pred. No. 2.2e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PNHFRPAGLPEKY 13

Db 110 PNHFRPAGLPEKY 122

RESULT 3  
SAA\_BOVIN  
ID SAA\_BOVIN STANDARD; PRT; 112 AA.  
AC P35541;  
DC 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Serum amyloid A protein (SAA) [Contains: Amyloid protein A (Amyloid  
GN fibril protein AA)].  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RX MEDLINE=92150985; PubMed=1738817;  
RA Rossevatn K., Andresen P.K., Sletten K., Husebekk A., Husby G.,  
RT Nordstoga K., Johnson K.H., Westmark G.T., Westmark P.;  
RL "The complete amino acid sequence of bovine serum amyloid protein A  
(SAA) and of subspecies of the tissue-deposited amyloid fibril  
protein A.";  
RN Scand. J. Immunol. 35:217-224(1992).  
RN [2]  
RP SEQUENCE OF 1-90.  
RX MEDLINE=89080450; PubMed=2909653;  
RA Benson M.D., Dibartola S.P., Dwulet F.E.;  
RL "A unique insertion in the primary structure of bovine amyloid AA  
protein.";  
RN J. Lab. Clin. Med. 113:67-72(1989).  
RN [3]  
RP SEQUENCE OF 4-16.  
RX MEDLINE=8827778; PubMed=3393848;  
RA Husebekk A., Husby G., Sletten K., Skogen B., Nordstoga K.;  
RL "Characterization of bovine amyloid proteins SAA and AA.";  
RN Scand. J. Immunol. 27:739-743(1988).  
RN [4]  
RP SEQUENCE OF 3-48.  
RX MEDLINE=87079535; PubMed=3791962;  
RA Westmark P., Johnson K.H., Westmark G.T., Sletten K., Hayden D.W.;  
RL "Bovine amyloid protein AA: isolation and amino acid sequence  
analysis.";  
RN Comp. Biochem. Physiol. 85B:609-614(1986).  
CC -1- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL  
COMPLEX.  
CC -1- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.  
CC -1- INDUCTION: UPON CYTOKINE STIMULATION.  
CC -1- PTM: THIS PROTEIN IS THE PRECURSOR OF AMYLOID PROTEIN A, WHICH IS  
FORMED BY THE REMOVAL OF RESIDUES FROM THE CARBOXYL END.  
CC -1- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE  
EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.  
CC THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS;  
CC THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.  
CC -1- SIMILARITY: BELONGS TO THE SAA FAMILY.  
CC InterPro: IPR000096; Serum\_amyloid\_A.  
DR Pfam: PF00277; SAA\_proteins; 1.  
DR PRINTS: PR00306; SERUMAMYL0ID.  
DR PRODOM: PD002112; Serum\_amyloid\_A; 1.  
DR PROSITE: PS00992; SAA; 1.  
DR Acute phase; Plasma; HDL; Amyloid; Pyrrolidone carboxylic acid.  
KW CHAIN 1 112 SERUM AMYLOID A PROTEIN.  
FT CHAIN 1 112 AMYLOID PROTEIN A.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 112 AA; 12603 MW; 66E88810D4D49D34 CRC64;  
Query Match 96.1%; Score 74; DB 1; Length 112;  
Best Local Similarity 92.3%; Pred. No. 6.6e-06;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN [1]
RN SEQUENCE.
RC TISSUE=Plasma;
RC MEDLINE=94120345; PubMed=8290897;
RA Syversen P.V., Juul J., Marhaug G., Husby G., Sletten K.;
RT "The primary structure of serum amyloid A protein in the sheep:
RT comparison with serum amyloid A in other species.";
RL Scand. J. Immunol. 39:88-94(1994).
CC -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC COMPLEX.
CC -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.
CC -!- INDUCTION: Upon cytokine stimulation.
CC -!- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE
CC EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.
CC THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS;
CC THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.
CC -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
CC InterPro: IPR000096; Serum_amyloid_A.
DR Pfam: PF00277; SAA_proteins.1.
DR PRINTS: PR00306; SERUMAMYLOID.
DR ProDom: PD002112; Serum_amyloid_A; 1.
DR SMART: SM00187; SAA; 1.
DR PROSITE: PS00992; SAA; 1.
DR Acute phase; Plasma; HDL; Amyloid; Pyrrolidone carboxylic acid.
FW MOD_RES 1 PYRROLIDONE CARBOXYLIC ACID.
KT SEQUENCE 112 AA; 12688 MW; 11A37FD59A8C1649 CRC64;
SQ
Query Match 89.6%; Score 69; DB 1; Length 112;
Best Local Similarity 84.6%; Pred. No. 4.9e-05;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 PNHFRPAGLPDKY 13
DB 100 PNHFRPGLPDKY 112

RESULT 10
SAA1_RABIT
ID SAA1_RABIT STANDARD; PRT; 122 AA.
AC P53614.
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Serum amyloid A-1 protein precursor.
GN SAA1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OC NCBI_TaxID=9986;
RN [1]
RN SEQUENCE FROM N.A.
RC MEDLINE=92086627; PubMed=1721234;
RA Rygg M., Marhaug G., Husby G., Dowton S.B.;
RT "Rabbit serum amyloid protein A: expression and primary structure
RT deduced from cDNA sequences.";
RL Scand. J. Immunol. 34:727-734(1991).
CC -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC COMPLEX.
CC -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER.
CC -!- INDUCTION: Upon cytokine stimulation.
CC -!- DISEASE: REACTIVE, SECONDARY AMYLOIDOSIS IS CHARACTERIZED BY THE
CC EXTRACELLULAR ACCUMULATION IN VARIOUS TISSUES OF THE SAA PROTEIN.
CC THESE DEPOSITS ARE HIGHLY INSOLUBLE AND RESISTANT TO PROTEOLYSIS;
CC THEY DISRUPT TISSUE STRUCTURE AND COMPROMISE FUNCTION.
CC -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
-----
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OM protein - protein search, using sw model

Run on: August 18, 2003, 01:10:58 ; Search time 67 Seconds  
(without alignments)  
50.070 Million cell updates/sec

Title: US-09-846-779-1

Perfect score: 77

Sequence: 1 PNHFRPAGLPEKY 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

otal number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL23:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phase:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_rvirus:\*

16: sp\_bacteriap:\*

17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	100.0	122	4	Q16834
2	74	96.1	131	6	Q8sq28
3	69	89.6	122	6	Q29514
4	68	88.3	128	6	Q9N0Y1
5	67	87.0	143	6	Q9WZT5
6	67	87.0	159	11	Q64423
7	66	85.7	111	6	Q9XSG7
8	60	77.9	122	11	Q8R3T4
9	60	77.9	122	11	Q64454
10	60	77.9	122	11	P97374
11	60	77.9	122	11	P97375
12	57	74.0	123	13	Q9YIA4
13	55	71.4	114	13	P79900
14	55	71.4	127	5	Q8WY11
15	53	68.8	122	5	Q9GSP8
16	52	67.5	129	13	Q8JIB0

#### ALIGNMENTS

RESULT 1

Q16834 PRELIMINARY; PRT; 122 AA.

AC Q16834;  
DT 01-NOV-1996 (TREMREL. 01, Created)  
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)  
DT 01-OCT-2002 (TREMREL. 22, Last annotation update)  
DE SAAB1 beta protein precursor (Serum amyloid A protein).  
GS SAAB1 BETA.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=92022342; PubMed=1656519;  
RA Betts J.C., Edbrooke M.R., Thakker R.V., Woo P.;  
RT "The human acute-phase serum amyloid A gene family: structure,  
RT evolution and expression in hepatoma cells.";  
RL Scand. J. Immunol. 34:471-482(1991).  
CC -I- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL  
CC COMPLEX (BY SIMILARITY).  
CC -I- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY  
CC SIMILARITY).  
CC -I- SIMILARITY: BELONGS TO THE SAA FAMILY.  
DR ENBL; X56652; CAA39974.1;  
DR InterPro; IPR000096; Serum\_amyloid\_A.  
DR Pfam; PF00277; SAA\_proteins; 1.  
DR PRINTS; PR00306; SERUMAMYL0ID.  
DR ProDom; PD002112; Serum\_amyloid\_A; 1.  
DR SMART; SM00197; SAA; 1.  
DR PROSITE; PS00992; SAA; 1.  
KW Acute phase; HDL; Signal.  
FT SIGNAL. 1 18  
FT CHAIN 19 122  
SQ SEQUENCE 122 AA; 13532 MW; D913BF06AA4107A2 CRC64;

Query Match 100.0%; Score 77; DB 4; Length 122;

Q9aul4 oryza sativ  
Q819l1 arabidopsis  
Q9lyb3 arabidopsis  
Q95wr8 caenorhabdi  
Q21218 caenorhabdi  
Q9twa9 drosophila  
Q81947 caenorhabdi  
Q81948 caenorhabdi  
Q8peg1 xylella fas  
Q8bsq4 mus musculu  
Q95938 rattus norv  
Q939x6 streptomyce  
Q61243 mus musculu  
Q9bde9 metarhizium  
Q9jvf9 neisseria m  
Q9jxh6 neisseria m  
Q95150 bos taurus  
Q8kaas chlorobium  
Q93709 sulfolobus  
Q97wy1 sulfolobus  
Q8qah1 arthrobacte  
Q31226 arthrobacte  
Q9w362 drosophila  
Q9lwk7 oryza sativ  
Q8fg07 escherichia  
Q48967 zea mays (m  
Q9f907 treponema p  
Q8pm20 xanthomonas  
Q96169 homo sapien

17 47 61.0 355 10 Q9AUL4  
18 46 59.7 404 10 Q819L1  
19 46 59.7 404 10 Q9LYB3  
20 46 59.7 1347 5 Q95WR8  
21 46 59.7 1470 5 Q21218  
22 45 58.4 88 5 Q9TWA9  
23 45 58.4 2329 5 Q81G47  
24 45 58.4 2747 5 Q81G48  
25 44 57.1 364 16 Q9PEG1  
26 44 57.1 921 11 Q8BSQ4  
27 43.5 56.5 514 8 Q95938  
28 43 55.8 306 2 Q93GX6  
29 42 54.5 123 11 Q61243  
30 42 54.5 737 3 Q9HDE9  
31 41 53.2 145 16 Q9JVF9  
32 41 53.2 152 16 Q9JXH6  
33 41 53.2 187 6 Q95150  
34 41 53.2 205 16 Q8KAA5  
35 41 53.2 413 1 Q93709  
36 41 53.2 414 17 Q97WY1  
37 41 53.2 429 2 Q8GAH1  
38 41 53.2 430 2 Q31226  
39 41 53.2 595 5 Q9W362  
40 41 53.2 622 10 Q9LWK7  
41 41 53.2 649 16 Q8FG07  
42 40.5 52.6 464 10 Q48967  
43 40 51.9 137 2 Q9F907  
44 40 51.9 229 16 Q8PM20  
45 40 51.9 233 4 Q96169

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Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNHFRPAGLPEKY 13
DB 110 PNHFRPAGLPEKY 122

RESULT 2
Q8SQ28 PRELIMINARY; PRT; 131 AA.
AC Q8SQ28;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Serum amyloid A3 isoform protein precursor (Serum amyloid A
DE protein).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
QX [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Mammary gland;
RX MEDLINE=21589074; PubMed=11730930;
RA McDonald T.L., Larson M.A., Mack D.R., Weber A.;
RT "Elevated extrahepatic expression and secretion of mammary-associated
serum amyloid A 3 (M-SAA3) into colostrum.";
RL Vet. Immunol. Immunopathol. 83:203-211(2001).
RN [2]
RN SEQUENCE FROM N.A.
RA Gutierrez-Pabello J.A., Barthel R., Adams G.;
RT "Differential gene expression of Mycobacterium bovis infected bovine
macrophages.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC COMPLEX (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR EMBL; AF335552; AAM11538.1; -.
DR EMBL; AF540564; AAM17326.1; -.
DR InterPro; IPR000096; Serum_amyloid_A.
DR Pfam; PF00277; SAA_proteins; 1.
DR ProDom; PD002112; Serum_amyloid_A; 1.
DR SMART; SM00197; SAA; 1.
DR PROSITE; PS00992; SAA; 1.
FT SIGNAL 1 18
FT CHAIN 19 131 SERUM AMYLOID A3 ISOFORM PROTEIN.
FT SEQUENCE 131 AA; 14723 MW; BB5F58F07A3B9331 CRC64;

Query Match 96.1%; Score 74; DB 6; Length 131;
Best Local Similarity 92.3%; Pred. No. 5.4e-05;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNHFRPAGLPEKY 13
DB 119 PNHFRPAGLPEKY 131

RESULT 3
Q29514 PRELIMINARY; PRT; 122 AA.
AC Q29514;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical serum amyloid A protein.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
```

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NCBI_TaxID=9986;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=91315474; PubMed=1859410;
RA Ray B.K., Ray A.;
RT "Molecular cloning and nucleotide sequence of complementary DNA
encoding rabbit alpha 1-acid glycoprotein.";
RL Biochem. Biophys. Res. Commun. 178:507-513(1991).
CC -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC COMPLEX (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR EMBL; X58728; CAA41560.1; -.
DR InterPro; IPR000096; Serum_amyloid_A.
DR Pfam; PF00277; SAA_proteins; 1.
DR PRINTS; PR00306; SERUMAMYLOID.
DR ProDom; PD002112; Serum_amyloid_A; 1.
DR SMART; SM00197; SAA; 1.
DR PROSITE; PS00992; SAA; 1.
KW Hypothetical protein; Acute phase; HDL.
SQ SEQUENCE 122 AA; 13509 MW; B635BEB22907945 CRC64;

Query Match 89.6%; Score 69; DB 6; Length 122;
Best Local Similarity 84.6%; Pred. No. 0.00036;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PNHFRPAGLPEKY 13
DB 110 PNHFRPAGLPEKY 122

RESULT 4
Q9NOY1 PRELIMINARY; PRT; 128 AA.
AC Q9NOY1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Serum amyloid A precursor (Serum amyloid A protein).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Liver;
RX MEDLINE=20579389; PubMed=11137129;
RA Ma Z., Mizukoshi T., Khatlani T.S., Okuda M., Onishi T.;
RT "Molecular cloning and sequencing of equine cDNA encoding serum
amyloid A (SAA)";
RL Vet. Immunol. Immunopathol. 77:321-327(2000).
CC -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC COMPLEX (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR EMBL; AF240364; AAF63164.1; -.
DR InterPro; IPR000096; Serum_amyloid_A.
DR Pfam; PF00277; SAA_proteins; 1.
DR PRINTS; PR00306; SERUMAMYLOID.
DR ProDom; PD002112; Serum_amyloid_A; 1.
DR SMART; SM00197; SAA; 1.
DR PROSITE; PS00992; SAA; 1.
KW Acute phase; HDL; Signal.
FT SIGNAL 1 18
FT SEQUENCE 128 AA; 14067 MW; CA8F4DF1DD2A33 CRC64;

Query Match 88.3%; Score 68; DB 6; Length 128;
Best Local Similarity 84.6%; Pred. No. 0.00057;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PNHFRPAGLPEKY 13
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||||| |||:|  
116 PNHFRPGLPKY 128

RESULT 5

Q9WZT5 PRELIMINARY; PRT; 143 AA.  
AC Q9WZT5;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Serum amyloid A protein.  
GN SAA3.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
C TISSUE=Mammary gland;  
RT "Cloning and characterization of involution-specific genes from the  
RT bovine mammary gland";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL  
CC COMPLEX (BY SIMILARITY).  
CC -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY  
CC SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE SAA FAMILY.  
DR EMBL: AF160867; AAF7630.1; .  
DR InterPro: IPR000096; Serum\_amyloid\_A.  
DR Pfam: PF00277; SAA\_proteins; 1.  
DR PRINTS: PR00306; SERUMAMYL0ID.  
DR ProDom: PD002112; Serum\_amyloid\_A; 1.  
DR SMART: SM00197; SAA; 1.  
DR PROSITE: PS00992; SAA; 1.  
KW Acute phase; HDL.  
SQ SEQUENCE 143 AA; 15819 MW; F32DE20B5A635D2C CRC64;

Query Match 87.0%; Score 67; DB 6; Length 143;  
Best Local Similarity 91.7%; Pred. No. 0.00094;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNHFRPAGLPEK 12  
||||| |||:|  
DB 119 PNHFRPAGLPEK 130

RESULT 6

Q64423 PRELIMINARY; PRT; 159 AA.  
AC Q64423;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Serum amyloid A protein.  
GN SAA3.  
OS Mesocricetus auratus (Golden hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Mesocricetus.  
OX NCBI\_TaxID=10036;  
RN [1]  
RP SEQUENCE FROM N.A.  
C TISSUE=Liver;  
RX MEDLINE=89352552; PubMed=2765510;  
RA Webb C.F., Tucker P.W., Dowton S.B.;  
RT "Expression and sequence analysis of serum amyloid a in the Syrian  
RT hamster";  
RL Biochemistry 28:4785-4790(1989).  
CC -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL  
CC COMPLEX (BY SIMILARITY).

-!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY  
CC SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE SAA FAMILY.  
DR EMBL: LJ3384; AAA37097.1; .  
DR EMBL: M27241; AAA37097.1; JOINED.  
DR EMBL: LJ3383; AAA37097.1; JOINED.  
DR InterPro: IPR000096; Serum\_amyloid\_A.  
DR Pfam: PF00277; SAA\_proteins; 1.  
DR PRINTS: PR00306; SERUMAMYL0ID.  
DR ProDom: PD002112; Serum\_amyloid\_A; 1.  
DR SMART: SM00197; SAA; 1.  
DR PROSITE: PS00992; SAA; 1.  
KW Acute phase; HDL.  
SQ SEQUENCE 159 AA; 17955 MW; 8B4787705E9940A5 CRC64;

Query Match 87.0%; Score 67; DB 11; Length 159;  
Best Local Similarity 84.6%; Pred. No. 0.0011;  
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PNHFRPAGLPEKY 13  
||||| |||:|  
DB 147 PNHFRPAGLPSKY 159

RESULT 7

Q9XSG7 PRELIMINARY; PRT; 111 AA.  
AC Q9XSG7;  
DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Serum amyloid A protein (Fragment).  
GN SAA.  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Onno K., Terado M., Iwata H., Inokuma H., Onishi T.;  
RT "Expression of recombinant feline serum amyloid A (SAA) protein.";  
RL J. Vet. Med. Sci. 0:0-0(1999).  
CC -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL  
CC COMPLEX (BY SIMILARITY).  
CC -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY  
CC SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE SAA FAMILY.  
DR EMBL: AF136718; AAD24489.1; .  
DR InterPro: IPR000096; Serum\_amyloid\_A.  
DR Pfam: PF00277; SAA\_proteins; 1.  
DR PRINTS: PR00306; SERUMAMYL0ID.  
DR ProDom: PD002112; Serum\_amyloid\_A; 1.  
DR SMART: SM00197; SAA; 1.  
DR PROSITE: PS00992; SAA; 1.  
KW Acute phase; HDL.  
FT NON\_TER 1  
SQ SEQUENCE 111 AA; 12547 MW; D9392BD358AF5D22 CRC64;

Query Match 85.7%; Score 66; DB 6; Length 111;  
Best Local Similarity 76.9%; Pred. No. 0.0011;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PNHFRPAGLPEKY 13  
||||| |||:|  
DB 99 PNHFRPAGLPEKY 111

RESULT 8

Q8R3T4 PRELIMINARY; PRT; 122 AA.  
ID Q8R3T4;  
AC Q8R3T4;  
DT 01-JUN-2002 (TREMBlrel. 21, Created)  
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

```
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to serum amyloid A 2 (Serum amyloid A protein).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Submitted R.;
RL Submitted (Mar-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC COMPLEX (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR EMBL; BC024606; AA24606.1; -.
DR InterPro; IPR000096; Serum_amyloid_A.
DR Pfam; PF00277; SAA_proteins; 1.
DR ProDom; PD002112; Serum_amyloid_A; 1.
DR SMART; SM00197; SAA; 1.
DR PROSITE; PS00992; SAA; 1.
KW Acute phase; HDL.
SQ SEQUENCE 122 AA; 13732 MW; 53F4A895D1DC15DB CRC64;

Query Match 77.9%; Score 60; DB 11; Length 122;
Best Local Similarity 69.2%; Pred. No. 0.013;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 PNHFRPAGLPEKY 13
|:::| |::|
DB 110 PNYRPPGLPKY 122

RESULT 9
Q64454 PRELIMINARY; PRT; 122 AA.
AC Q64454;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Serum amyloid A protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA de Beer M.C., de Beer F.C., McCubbin W.D., Kay C.M., Kindy M.S.;
RL "Structural prerequisites for serum amyloid A fibril formation.";
J. Biol. Chem. 268:20606-20612(1993).
CC -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC COMPLEX (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR EMBL; L22190; AAA19818.1; -.
DR InterPro; IPR000096; Serum_amyloid_A.
DR Pfam; PF00277; SAA_proteins; 1.
DR PRINTS; PR00306; SERUMAMYL0ID.
DR ProDom; PD002112; Serum_amyloid_A; 1.
DR SMART; SM00197; SAA; 1.
DR PROSITE; PS00992; SAA; 1.
KW Acute phase; HDL.
SQ SEQUENCE 122 AA; 13700 MW; FAA291682A8F770A CRC64;

Query Match 77.9%; Score 60; DB 11; Length 122;
Best Local Similarity 69.2%; Pred. No. 0.013;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 PNHFRPAGLPEKY 13
|:::| |::|
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DB 110 PNYRPPGLPKY 122

RESULT 10
P97374 PRELIMINARY; PRT; 122 AA.
AC P97374;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Serum amyloid A protein isoform 1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Cathcart E., Carreras I., Elliott-Bryant R., Liang J.S.,
RA Gonnerman W.A., Sipe J.;
RT "Polymorphisms of Acute Phase Serum Amyloid A Isoforms and Amyloid
RT Resistance in Wild-type Mus musculus Czech.";
Clin. Immunol. Immunopathol. 0:0-0(1996).
RL Clin. Immunol. Immunopathol. 0:0-0(1996).
CC -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC COMPLEX (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR EMBL; U60437; AAB37249.1; -.
DR MGD; MGI:98222; Saa2.
DR InterPro; IPR000096; Serum_amyloid_A.
DR Pfam; PF00277; SAA_proteins; 1.
DR PRINTS; PR00306; SERUMAMYL0ID.
DR ProDom; PD002112; Serum_amyloid_A; 1.
DR SMART; SM00197; SAA; 1.
DR PROSITE; PS00992; SAA; 1.
KW Acute phase; HDL.
SQ SEQUENCE 122 AA; 13732 MW; 09EB8AA8CE1B43E CRC64;

Query Match 77.9%; Score 60; DB 11; Length 122;
Best Local Similarity 69.2%; Pred. No. 0.013;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 PNHFRPAGLPEKY 13
|:::| |::|
DB 110 PNYRPPGLPKY 122

RESULT 11
P97375 PRELIMINARY; PRT; 122 AA.
AC P97375;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Serum amyloid A protein isoform 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Cathcart E., Carreras I., Elliott-Bryant R., Liang J.S.,
RA Gonnerman W.S., Sipe J.;
RT "Polymorphism of Acute Phase Serum Amyloid A Isoforms and Amyloid
RT Resistance in Wild-type Mus musculus Czech.";
Clin. Immunol. Immunopathol. 0:0-0(1996).
RL Clin. Immunol. Immunopathol. 0:0-0(1996).
CC -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC COMPLEX (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
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CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR EMBL; U60438; AAB37250.1; -.
DR MGD; MG1:98222; Saa2.
DR InterPro; IPR000096; Serum_amyloid_A.
DR Pfam; PF00277; SAA_proteins; 1.
DR PRINTS; PR00306; SERUMAMYL0ID.
DR ProDom; PD002112; Serum_amyloid_A; 1.
DR SMART; SM00197; SAA; 1.
DR PROSITE; PS00992; SAA; 1.
KW Acute phase; HDL.
SQ SEQUENCE 122 AA; 13638 MW; EEE79A1FE0432022 CRC64;

Query Match 77.98; Score 60; DB 11; Length 122;
Best Local Similarity 69.28; Pred. No. 0.013;
Matches 9; Conservative 3; Mismatches 0; Gaps 0;

OY 1 PNHRFPAGLPKY 13
Gb 110 PNYRPPGLPKY 122

RESULT 12
Q9YIA4
ID Q9YIA4 PRELIMINARY; PRT; 123 AA.
AC Q9YIA4;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Serum amyloid A protein.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20394649; PubMed=10938736;
RA Fujiki K., Shin D.H., Nakao M., Yano T.;
RT "Molecular cloning and expression analysis of carp (Cyprinus carpio)
RT interleukin-beta, high affinity immunoglobulin E Fc receptor gamma
RT subunit and serum amyloid A."
RL Fish and Shellfish Immunol. 10:229-242(2000).
RC -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC -!- COMPLEX (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR EMBL; AB016524; BAA36700.1; -.
DR InterPro; IPR000096; Serum_amyloid_A.
DR Pfam; PF00277; SAA_proteins; 1.
DR PRINTS; PR00306; SERUMAMYL0ID.
DR ProDom; PD002112; Serum_amyloid_A; 1.
DR SMART; SM00197; SAA; 1.
DR PROSITE; PS00992; SAA; 1.
KW Acute phase; HDL.
SQ SEQUENCE 123 AA; 13777 MW; B364917D3B2C4B8A CRC64;

Query Match 74.08; Score 57; DB 13; Length 123;
Best Local Similarity 69.28; Pred. No. 0.042;
Matches 9; Conservative 2; Mismatches 0; Gaps 0;

OY 1 PNHRFPAGLPKY 13
Db 111 PNYRPPGLPKY 123

RESULT 13
P79900
ID P79900 PRELIMINARY; PRT; 114 AA.
AC P79900;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)

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DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Acute phase serum amyloid A (SAA) precursor (Serum amyloid A protein)
DE (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RX MEDLINE=97131713; PubMed=9977214;
RA Jensen L.E., Hiney M.P., Shields D.C., Uhlar C.M., Lindsey A.J.;
RA Whitehead A.S.;
RT "Acute phase proteins in salmonids. Evolutionary analyses and acute
RT phase response."
RL J. Immunol. 158:384-392(1997).
CC -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC -!- COMPLEX (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR EMBL; X99387; CAA67766.1; -.
DR InterPro; IPR000096; Serum_amyloid_A.
DR Pfam; PF00277; SAA_proteins; 1.
DR PRINTS; PR00306; SERUMAMYL0ID.
DR ProDom; PD002112; Serum_amyloid_A; 1.
DR SMART; SM00197; SAA; 1.
DR PROSITE; PS00992; SAA; 1.
KW Acute phase; HDL; Signal.
FT NON_TER 1
FT SIGNAL 11
FT CHAIN 12 114
SQ SEQUENCE 114 AA; 12693 MW; 02D96C6F2ABE232C CRC64;

Query Match 71.48; Score 55; DB 13; Length 114;
Best Local Similarity 69.28; Pred. No. 0.086;
Matches 9; Conservative 1; Mismatches 0; Gaps 0;

OY 1 PNHRFPAGLPKY 13
Db 102 PNRFRPQGLPKNY 114

RESULT 14
Q8MY11
ID Q8MY11 PRELIMINARY; PRT; 127 AA.
AC Q8MY11;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Amyloid protein A.
GN AMPAA.
OS Branchiostoma belcheri (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7741;
RN [1]
RP SEQUENCE FROM N.A.
RA Kubokawa K.;
RT "Characterization of amyloid protein A in amphioxus."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB079688; BAB97379.1; -.
DR InterPro; IPR000096; Serum_amyloid_A.
DR Pfam; PF00277; SAA_proteins; 1.
DR PRINTS; PR00306; SERUMAMYL0ID.
DR ProDom; PD002112; Serum_amyloid_A; 1.
DR SMART; SM00197; SAA; 1.
SQ SEQUENCE 127 AA; 14114 MW; 90C69A8FD98ECC2F CRC64;

Query Match 71.48; Score 55; DB 5; Length 127;
Best Local Similarity 61.58; Pred. No. 0.097;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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QY 1 PNHFRPAGLPKEY 13  
 II :II :II :I  
 Db 115 PNYRPEGLPDY 127

RESULT 15

QGSP8 PRELIMINARY; PRT; 122 AA.  
 AC QGSP8; 2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE Serum amyloid A protein.  
 OS Holothuria glaberrima.  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Holothuroidea; Aspidochiroidea; Aspidochiroidea; Holothuriidae;  
 OC Holothuria.  
 OX NCBI\_TaxID-31192;  
 {}  
 . SEQUENCE FROM N.A.  
 RA Santiago-Cardona P.G., Roig-Lopez J.L., Santiago C.L.,  
 RA Garcia-Ararras J.E.;  
 RT "Holothuroid serum amyloid A protein."  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF300706; RAG24633.1; -  
 DR InterPro: IPR000096; Serum\_amyloid\_A.  
 DR Pfam: PF00277; SAA\_proteins; 1.  
 DR PRINTS: PR00306; SERUMAMYLOID.  
 DR ProDom: PD002112; Serum\_amyloid\_A; 1.  
 DR SMART: SM00197; SAA; 1.  
 DR PROSITE: PS00992; SAA; 1.  
 SQ SEQUENCE 122 AA; 13580 MW; 740FCE6C8661FD8B CRC64;

Query Match 68.8%; Score 53; DB 5; Length 122;  
 Best Local Similarity 69.2%; Pred. No. 0.2;  
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 PNHFRPAGLPKEY 13  
 II :II :II :I  
 Db 110 PNYRPPGLPSKY 122

Search completed: August 18, 2003, 01:26:21  
 Job time : 72 secs